#6

```
     ATGTGGAAATGGATACTGACACATTGTGCCTCAGCCTTTCCCCACCTGCCCGGCTGCTGC
  1  ---------+---------+---------+---------+---------+---------+   60
     TACACCTTTACCTATGACTGTGTAACACGGAGTCGGAAAGGGGTGGACGGGCCGACGACG

      M  W  K  W  I  L  T  H  C  A  S  A  F  P  H  L  P  G  C  C

     TGCTGCTGCTTTTTGTTGCTGTTCTTGGTGTCTTCCGTCCCTGTCACCTGCCAAGCCCTT
 61  ---------+---------+---------+---------+---------+---------+  120
     ACGACGACGAAAAACAACGACAAGAACCACAGAAGGCAGGGACAGTGGACGGTTCGGGAA

      C  C  C  F  L  L  L  F  L  V  S  S  V  P  V  T  C  Q  A  L

     GGTCAGGACATGGTGTCACCAGAGGCCACCAACTCTTCTTCCTCCTCCTTCTCCTCTCCT
121  ---------+---------+---------+---------+---------+---------+  180
     CCAGTCCTGTACCACAGTGGTCTCCGGTGGTTGAGAAGAAGGAGGAGGAAGAGGAGAGGA

      G  Q  D  M  V  S  P  E  A  T  N  S  S  S  S  S  F  S  S  P

     TCCAGCGCGGGAAGGCATGTgCGGAGCTACAATCACCTTCAAGGAGATGTCCGCTGGAGA
181  ---------+---------+---------+---------+---------+---------+  240
     AGGTCGCGCCCTTCCGTACAcGCCTCGATGTTAGTGGAAGTTCCTCTACAGGCGACCTCT

      S  S  A  G  R  H  V  R  S  Y  N  H  L  Q  G  D  V  R  W  R
```

MATCH WITH FIG. 1B

FIG.1A

MATCH WITH FIG. 1A

```
     AAGCTATTCTCTTTCACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGGTCAGCGGG
241  ---------+---------+---------+---------+---------+---------+  300
     TTCGATAAGAGAAAGTGGTTCATGAAAGAGTTCTAACTCTTCTTGCCCTTCCAGTCGCCC

      K  L  F  S  F  T  K  Y  F  L  K  I  E  K  N  G  K  V  S  G

     ACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT
301  ---------+---------+---------+---------+---------+---------+  360
     TGGTTCTTCCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA

      T  K  K  E  N  C  P  Y  S  I  L  E  I  T  S  V  E  I  G  V

     GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC
361  ---------+---------+---------+---------+---------+---------+  420
     CAACGGCAGTTTCGGTAATTGTCGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAG

      V  A  V  K  A  I  N  S  N  Y  Y  L  A  M  N  K  K  G  K  L

     TATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA
421  ---------+---------+---------+---------+---------+---------+  480
     ATACCGAGTTTTCTTAAATTGTTACTGACATTCGACTTCCTCTCCTATCTCCTTTTACCT

      Y  G  S  K  E  F  N  N  D  C  K  L  K  E  R  I  E  E  N  G
```

MATCH WITH FIG. 1C

FIG.1B

MATCH WITH FIG. 1B

```
     TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG
481  ---------+---------+---------+---------+---------+---------+  540
     ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCCGTTTACATACACCGTAAC

      Y  N  T  Y  A  S  F  N  W  Q  H  N  G  R  Q  M  Y  V  A  L

     AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC
541  ---------+---------+---------+---------+---------+---------+  600
     TTACCTTTTCCTCGAGGTTCCTCTCCTGTCTTTTGTGCTTCCTTTTTGTGGAGACGAGTG

      N  G  K  G  A  P  R  R  G  Q  K  T  R  R  K  N  T  S  A  H

     TTTCTTCCAATGGTGGTACACTCATAG
601  ---------+---------+-------    627
     AAAGAAGGTTACCACCATGTGAGTATC

      F  L  P  M  V  V  H  S  *
```

FIG. 1C

	1				50
FGF4	MS.GPGTAAV	ALLPAVLLAL	LA........	.PWAGRGGAA	APTAPNGTLE
FGF6	MSRGAGRLQG	TLWALVFLGI	LV........	.GMVVPSPAG	TR.ANNTLLD
FGF5	.......MSL	SFLLLLFFSH	LILSAWAHGE	KRLAPKGQPG	PAATDRNPIG
FGF1	....	....	....	....	....
FGF2	....	....	....	....	....
FGF9	....	....	....	..MAPLGEVG	NYFGVQDAVP
FGF7	....	......**MHKW**	**ILTWILPTLL**	.....YRS**CF**	HIIC**LVGTIS**
KGF2	....	......***MWKW***	***ILTHCASAFP***	*HLPGCCCC**CF***	*LLLFLVSSVP*
FGF3	....	....	....	.......MGL	IWLLLLSLLE
FGF8	MGSPRSALSC	LLLHLLVLCL	QAQVRSAAQK	RGPGAGNPAD	TLGQGHEDRP

	51				100
FGF4	AELERRWESL	VALSLARLPV	AA..QPKEAA	VQSGAGDY..	...**LLGIKRL**
FGF6	S...RGWGTL	LSRSRAGLAG	EI......AG	VNWESG.Y..	...**LVGIKRQ**
FGF5	SSSRQSSSSA	MSSSSASSSP	AASLGSQGSG	LEQSSFQW..	...SPSGRRT
FGF1	......MAEG	EITTFTALTE	KFN...LPPG	.......N..	...YK...KP
FGF2	......MAAG	SITTLPALPE	DGGSGAFPPG	.......**H**..	...FK...DP
FGF9	FGNVPVLPVD	SPVLLSDHLG	QSEAGGLPRG	PAVTDLDH..	...LKGILRR
FGF7	LACNDMTPEQ	M...**ATNVNC**	......**SSPE**	**RHTRSYDY**..	...**MEGGDIR**
KGF2	*VTCQALGQDM*	*VSPEATNSSS*	*SSFSSPSSAG*	***RHVRSYNH***..	...***LQ.GDVR***
FGF3	PGWPAAGPGA	....	...RLRRDAG	GRGGVYEH..	...**L.GGAPR**
FGF8	FGQRSRAGKN	FTNPAPNYPE	EGSKEQRDSV	LPKVTQRHVR	EQSLVTDQLS

MATCH WITH FIG. 2B

FIG.2A

MATCH WITH FIG. 2A

	101				150
FGF4	RRL.....YC	NVGIGFHLQA	LPDGRIGGAH	ADT.RDSLLE	LSPVERGV.V
FGF6	RRL.....YC	NVGIGFHLQV	LPDGRISGTH	EEN.PYSLLE	ISTVERGV.V
FGF5	GSL.....YC	RVGIGFHLQI	YPDGKVNGSH	EAN.MLSVLE	IFAVSQGI.V
FGF1	KLL.....YC	SNG.GHFLRI	LPDGTVDGTR	DRSDQHIQLQ	LSAESVGE.V
FGF2	KRL.....YC	KNG.GFFLRI	HPDGRVDGVR	EKSDPHIKLQ	LQAEERGV.V
FGF9	RQL.....YC	R.T.GFHLEI	FPNGTIQGTR	KDHSRFGILE	FISIAVGL.V
FGF7	VRR.....LF	CRT.QWYLRI	DKRGKVKGTQ	EMKNNYNIME	IRTVAVGI.V
KGF2	*WRK.....LF*	*SFT.KYFLKI*	*EKNGKVSGTK*	*KENCPYSILE*	*ITSVEIGV.V*
FGF3	RRK.....LY	CAT.KYHLQL	HPSGRVNGSL	.ENSAYSILE	ITAVEVGI.V
FGF8	RRLIRTYQLY	SRTSGKHVQV	LANKRINAMA	EDGDPFAKLI	VETDTFGSRV

	151				200
FGF4	SIFGVASRFF	VAMSSKGKLY	G.SPFFTDEC	TFKEILLPNN	YNAYESYKYP
FGF6	SLFGVRSALF	VAMNSKGRLY	A.TPSFQEEC	KFRETLLPNN	YNAYESDLYQ
FGF5	GIRGVFSNKF	LAMSKKGKLH	A.SAKFTDDC	KFRERFQENS	YNTYASAIHR
FGF1	YIKSTETGQY	LAMDTDGLLY	G.SQTPNEEC	LFLERLEENH	YNTYISKKH.
FGF2	SIKGVCANRY	LAMKEDGRLL	A.SKCVTDEC	FFFERLESNN	YNTYRSRKY.
FGF9	SIRGVDSGLY	LGMNEKGELY	G.SEKLTQEC	VFREQFEENW	YNTYSSNLYK
FGF7	AIKGVESEFY	LAMNKEGKLY	A.KKECNEDC	NFKELILENH	YNTYAS....
KGF2	*AVKAINSNYY*	*LAMNKKGKLY*	*G.SKEFNNDC*	*KLKERIEENG*	*YNTYAS....*
FGF3	AIRGLFSGRY	LAMNKRGRLY	A.SEHYSAEC	EFVERIHELG	YNTYASRLYR
FGF8	RVRGAETGLY	ICMNKKGKLI	AKSNGKGKDC	VFTEIVLENN	YTALQNAKY.

MATCH WITH FIG. 2C

FIG.2B

MATCH WITH FIG. 2B

	201				250
FGF4	....	GM......FI	ALSKNGKTKK	G..NRVSPTM	KVTHFLPRL.
FGF6	....	GT......YI	ALSKYGRVKR	G..SKVSPIM	TVTHFLPRI.
FGF5	....	TEKTGREWYV	ALNKRGKAKR	GCSPRVKPQH	ISTHFLPRFK
FGF1	....	...AEKNWFV	GLKKNGSCKR	G..PRTHYGQ	KAILFLPLPV
FGF2	....	...T..SWYV	ALKRTGQYKL	G..SKTGPGQ	KAILFLPMSA
FGF9	HV........	..DTGRRYYV	ALNKDGTPRE	G..TRTKRHQ	KFTHFLPRPV
FGF7	.......AKW	THNGGEM.FV	ALNQKGIPVR	G..KKTKKEQ	KTAHFLPMAI
KGF2	.......*FNW*	*QHNGRQM.YV*	*ALNGKGAPRR*	*G..QKTRRKN*	*TSAHFLPMVV*
FGF3	TVSSTPGARR	QPSAERLWYV	SVNGKGRPRR	G..FKTRRTQ	KSSLFLPRVL
FGF8	....	.....EGWYM	AFTRKGRPRK	G..SKTRQHQ	REVHFMKRLP

	251				300
FGF4	....	....	....	....	....
FGF6	....	....	....	....	....
FGF5	QSEQPELSFT	VTVPEKKNPP	SPIKSKIPLS	APRKNTNSVK	YRLKFRFG..
FGF1	SSD.......	....	....	....	....
FGF2	KS........	....	....	....	....
FGF9	DPDKVPELYK	DILSQS....	....	....	....
FGF7	T.........	....	....	....	....
KGF2	*HS*........	....	....	....	....
FGF3	DHRDHEMVRQ	LQSGLPRPPG	KGVQPRRRRQ	KQSPDNLEPS	HVQASRLGSQ
FGF8	RGHHTTEQSL	RFEFLNYPPF	TRSLRGSQRT	WAPEPR....	....

MATCH WITH FIG. 2D

FIG.2C

MATCH WITH FIG. 2C

	301
FGF4	......
FGF6	......
FGF5	......
FGF1	......
FGF2	......
FGF9	......
FGF7	......
KGF2	......
FGF3	LEASAH
FGF8	......

FIG.2D

GGAATTCCGG GAAGAGAGGG AAGAAAACAA CGGCGACTGG GCAGCTGCCT CCACTTCTGA 60

CAACTCCAAA GGGATATACT TGTAGAAGTG GCTCGCAGGC TGGGGCTCCG CAGAGAGAGA 120

CCAGAAGGTG CCAACCGCAG AGGGGTGCAG ATATCTCCCC CTATTCCCCA CCCCACCTCC 180

CTTGGGTTTT GTTCACCGTG CTGTCATCTG TTTTTCAGAC CTTTTTGGCA TCTAACATGG 240

TGAAGAAAGG AGTAAAGAAG AGAACAAAGT AACTCCTGGG GGAGCGAAGA GCGCTGGTGA 300

CCAACACCAC CAACGCCACC ACCAGCTCCT GCTGCTGCGG CCACCCACGT CCACCATTTA 360

CCGGGAGGCT CCAGAGGCGT AGGCAGCGGA TCCGAGAAAG GAGCGAGGGG AGTCAGCCGG 420

CTTTTCCGAG GAGTTATGGA TGTTGGTGCA TTCACTTCTG GCCAGATCCG CGCCCAGAGG 480

GAGCTAACCA GCAGCCACCA CCTCGAGCTC TCTCCTTGCC TTGCATCGGG TCTTACCCTT 540

CCAGTATGTT CCTTCTGATG AGACAATTTC CAGTGCCGAG AGTTTCAGTA CA ATG 595
Met

TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG CCC 643
Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro

GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC GTC 691
Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val

CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG GCC 739
Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala

ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA AGG 787
Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg

CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA AAG 835
His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys

CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG AAG 883
Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys

GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA 931
Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile

ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC 979
Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn

TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA 1027
Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu

TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC 1075
Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr

FIG.3A

AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT 1123
Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr

GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA 1171
Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg

AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA 1216
Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser

TAGAGGAAGG CAACGTTTGT GGATGCAGTA AAACCAATGG CTCTTTTGCC AAGAATAGTG 1276

GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC 1336

TTAAAAGAAA GCCAGCCTTT GAAGGTTTTT GTATTCACTG CTGACATATG ATGTTCTTTT 1396

AATTAGTTCT GTGTCATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT 1456

ATTCCCAAGT GAAAAACATT GTGGCTGGGT TTTTTGTTGT TGTTGTCAAG TTTTTGTTTT 1516

TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAATCT GTTGAAAGAA CGATCTTCGG 1576

GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT 1636

GAATCAATGA ACAGTAATAC GTGCAAGCAT TTACTGGAAA GCACTTGGGT CATATCATAT 1696

GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTTAAAAATA 1756

TAAACATGTT AGTGTGAAAC TGTTCTAACA ATACAAATAG TATGGTATGC TTGTGCATTC 1816

TGCCTTCATC CCTTTCTATT TCTTTCTAAG TTATTTATTT AATAGGATGT TAAATATCTT 1876

TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTTCT TTTTATTCAG 1936

CACACCACAT GCATGTTCAC GACAAAGTGT TTTTAAAACT TGGCGAACAC TTCAAAAATA 1996

GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTTGCA 2056

CTTCTGCAGT AATAACCATC AACAATAAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG 2116

AGATGTCTGC TATCATTTGA AAACATATAT TACTCTCGAG GCTTCCTGTC TCAAGAAATA 2176

GACCAGAAGG CCAAATTCTT CTCTTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA 2236

AAAAGGAAAA TTAATTGCTA AATACATTTA AATAGCCTAG CCTCATTATT TACTCATGAT 2296

TTCTTGCCAA ATGTCATGGC GGTAAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA 2356

TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT 2416

FIG.3B

CCCAGGGGCT TAAACTGAGC AAATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA 2476
AACCTGTTCT AGCTGTATGA TCTAGTCTTT ACAAAACCAA ATAAAACTTG TTTTCTGTAA 2536
ATTTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCATT TTGTTAGAGC 2596
ACGTATAGAA AAGAGTACAT AAGAGTTTAC CAATCATCAT CACATTGTAT TCCACTAAAT 2656
AAATACATAA GCCTTATTTG CAGTGTCTGT AGTGATTTTA AAAATGTAGA AAAATACTAT 2716
TTGTTCTAAA TACTTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT 2776
CATATTTCTT GTTTTGAAAA AGCATTTTAT TGTTTGGACA CAGTATTTTG GTACAAAAAA 2836
AAAGACTCAC TAAATGTGTC TTACTAAAGT TTAACCTTTG GAAATGCTGG CGTTCTGTGA 2896
TTCTCCAACA AACTTATTTG TGTCAATACT TAACCAGCAC TTCCAGTTAA TCTGTTATTT 2956
TTAAAAATTG CTTTATTAAG AAATTTTTTG TATAATCCCA TAAAAGGTCA TATTTTTCCC 3016
ATTCTTCAAA AAAACTGTAT TTCAGAAGAA ACACATTTGA GGCACTGTCT TTTGGCTTAT 3076
AGTTTAAATT GCATTTCATC ATACTTTGCT TCCAACTTGC TTTTTGGCAA ATGAGATTAT 3136
AAAAATGTTT AATTTTTGTG GTTGGAATCT GGATGTTAAA ATTTAATTGG TAACTCAGTC 3196
TGTGAGCTAT AATGTAATGC ATTCCTATCC AAACTAGGTA TCTTTTTTTC CTTTATGTTG 3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCCA CAACCTAAAT TAAATGTTTG 3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAAA CAGGGCACAA ACTGGATTCT 3376
TATTTCACAT AGACATTTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG 3436
TACTCAAGAC ACTAAAACAG CTTCTAGCCA AATATATTAA AGCTTGCAGA GGCCAAAAAT 3496
AGAAAACATC TCCCCTGTCT CTCCCACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG 3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTTGGGAGA CTGTGGGAAG ATGGCTTGAG 3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA 3676
AAACAAAACA AATGTAGCCA TGCGTGGTGG CATATACCTG TGGTCCCAAC TACTCAGGAG 3736
GCTGAAACGG AAGGATCTCT TGGGCCCCAG GAGTTTGAGG CTGCAGTGAG CTATAATCTT 3796
GCCATTGCAC TCCAGCCTGG GTGAAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA 3856
AAAGAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA 3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA 3976
GATTGTTTGG TAAGGAGTAA TGACATTCTC TTGCATTTAA AAGTGGCATA TTTGCTTGAA 4036

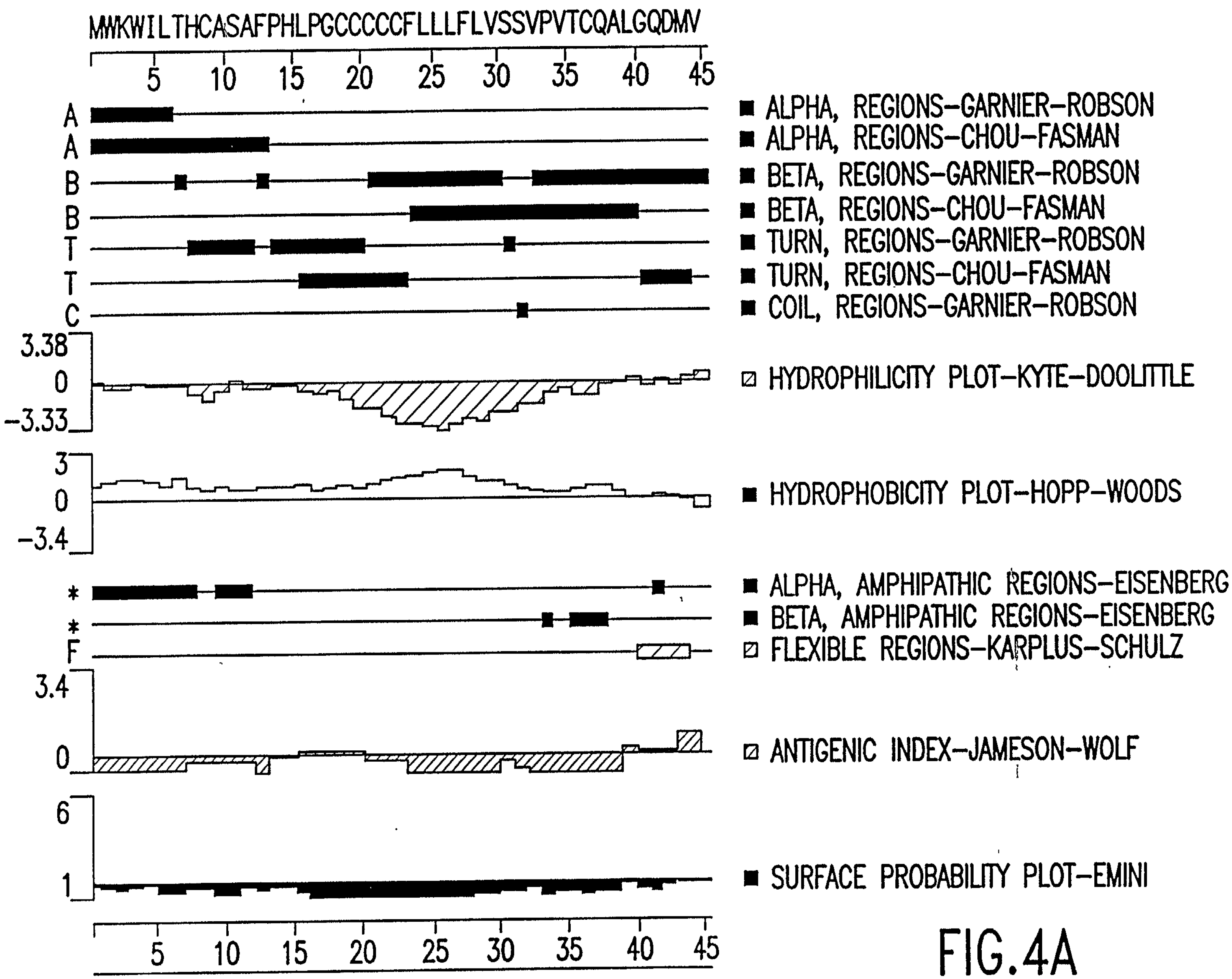
FIG.3C

ATGGAAATAG AATTCTGGTC CCTTTTGCAA CTACTGAAGA AAAAAAAAAG CAGTTTCAGC 4096

CCTGAATGTT GTAGATTTGA AAAAAAAAAA AAAAAAACTC GAGGGGGGGC CCGTACCCAA 4156

TTCGCCCTAT AGTGAGTCGT A 4177

FIG.3D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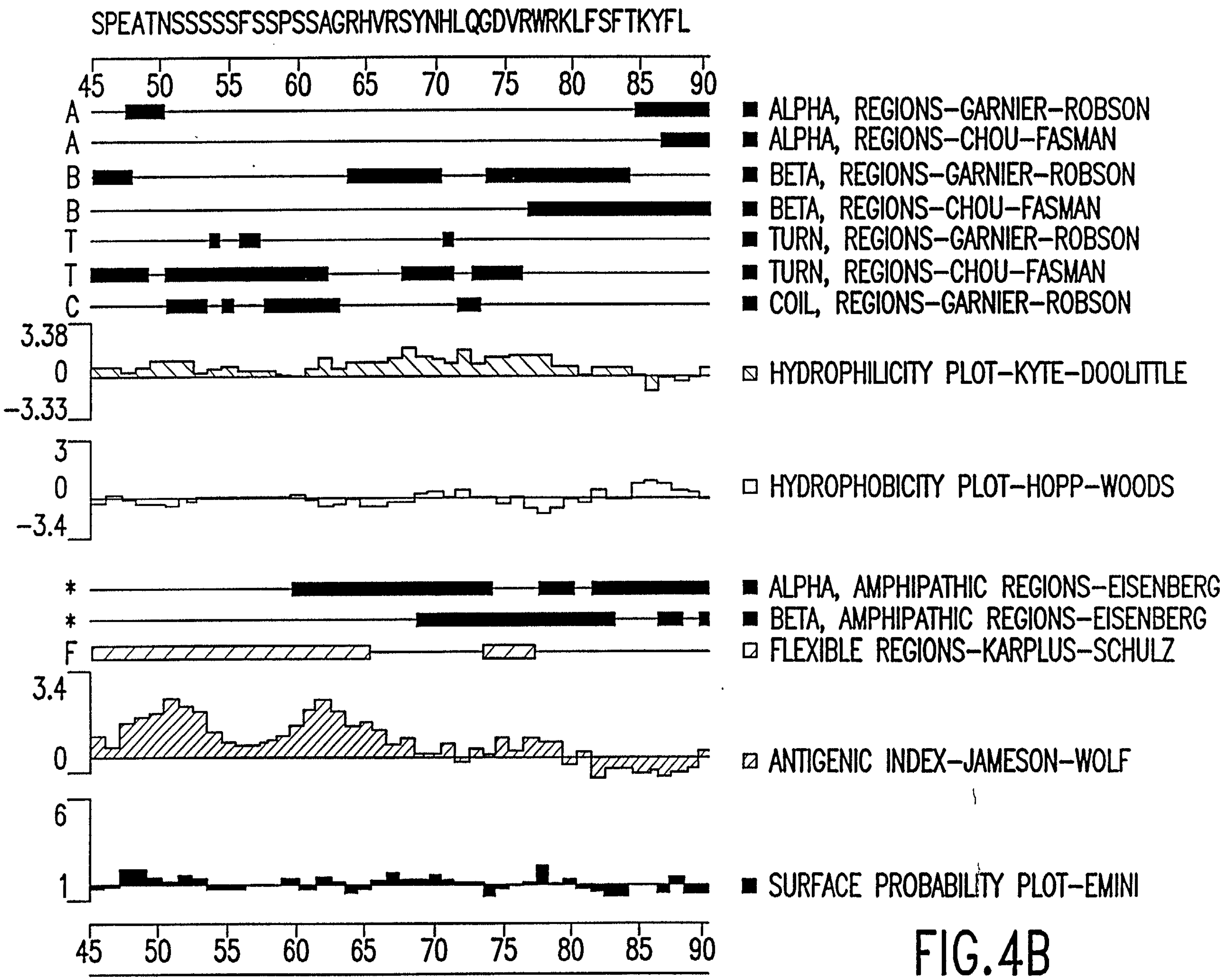
5 10 15 20 25 30 35 40 45
A
A
B
B
T
T
C
ALPHA, REGIONS–GARNIER–ROBSON
ALPHA, REGIONS–CHOU–FASMAN
BETA, REGIONS–GARNIER–ROBSON
BETA, REGIONS–CHOU–FASMAN
TURN, REGIONS–GARNIER–ROBSON
TURN, REGIONS–CHOU–FASMAN
COIL, REGIONS–GARNIER–ROBSON
3.38
0
–3.33
HYDROPHILICITY PLOT–KYTE–DOOLITTLE
3
0
–3.4
HYDROPHOBICITY PLOT–HOPP–WOODS
*
*
F
ALPHA, AMPHIPATHIC REGIONS–EISENBERG
BETA, AMPHIPATHIC REGIONS–EISENBERG
FLEXIBLE REGIONS–KARPLUS–SCHULZ
3.4
0
ANTIGENIC INDEX–JAMESON–WOLF
6
1
SURFACE PROBABILITY PLOT–EMINI
5 10 15 20 25 30 35 40 45

FIG.4A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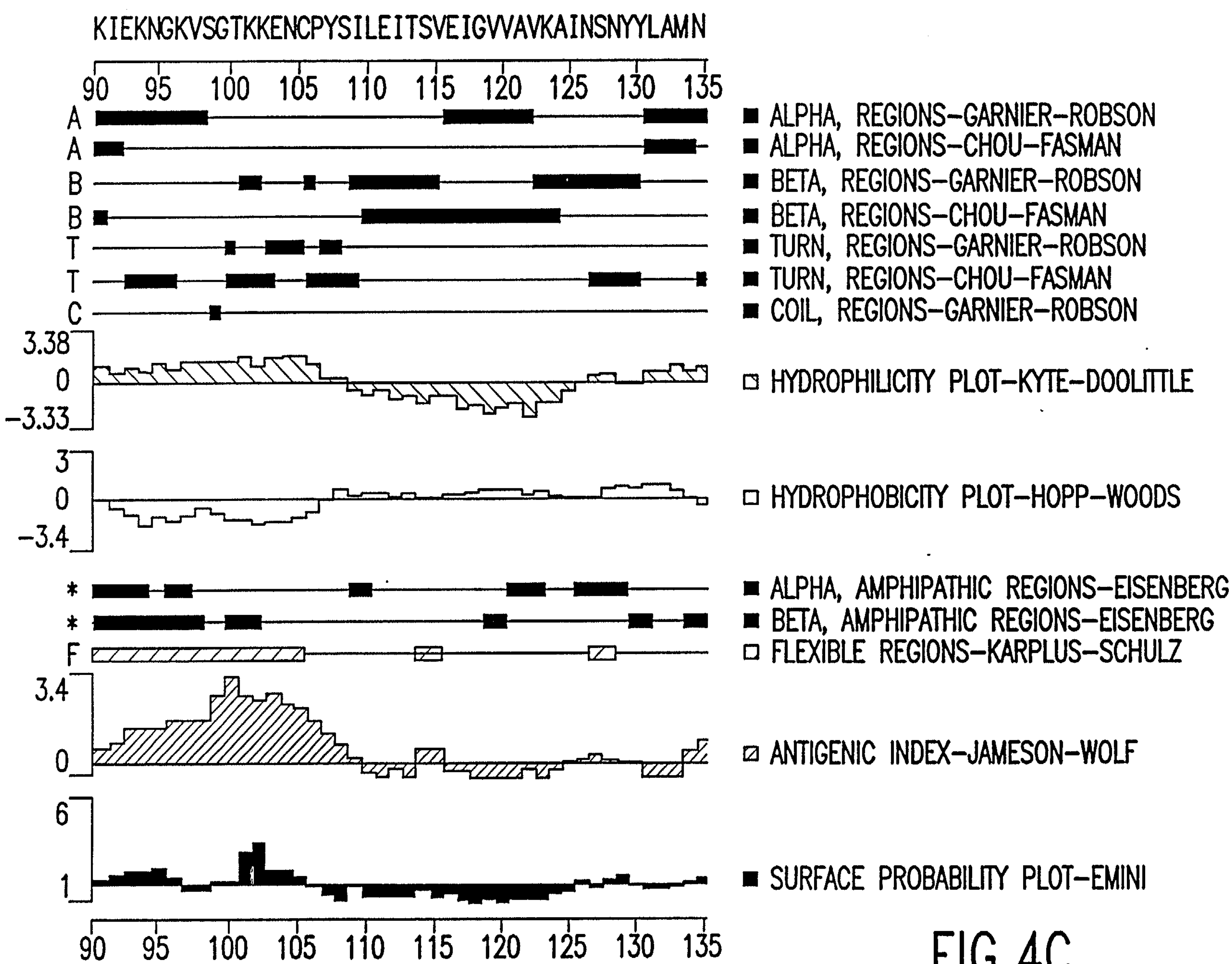
A
A
B
B
T
T
C
3.38
0
-3.33
3
0
-3.4
*
*
F
3.4
0
6
1
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
HYDROPHOBICITY PLOT-HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
ANTIGENIC INDEX-JAMESON-WOLF
SURFACE PROBABILITY PLOT-EMINI

FIG.4B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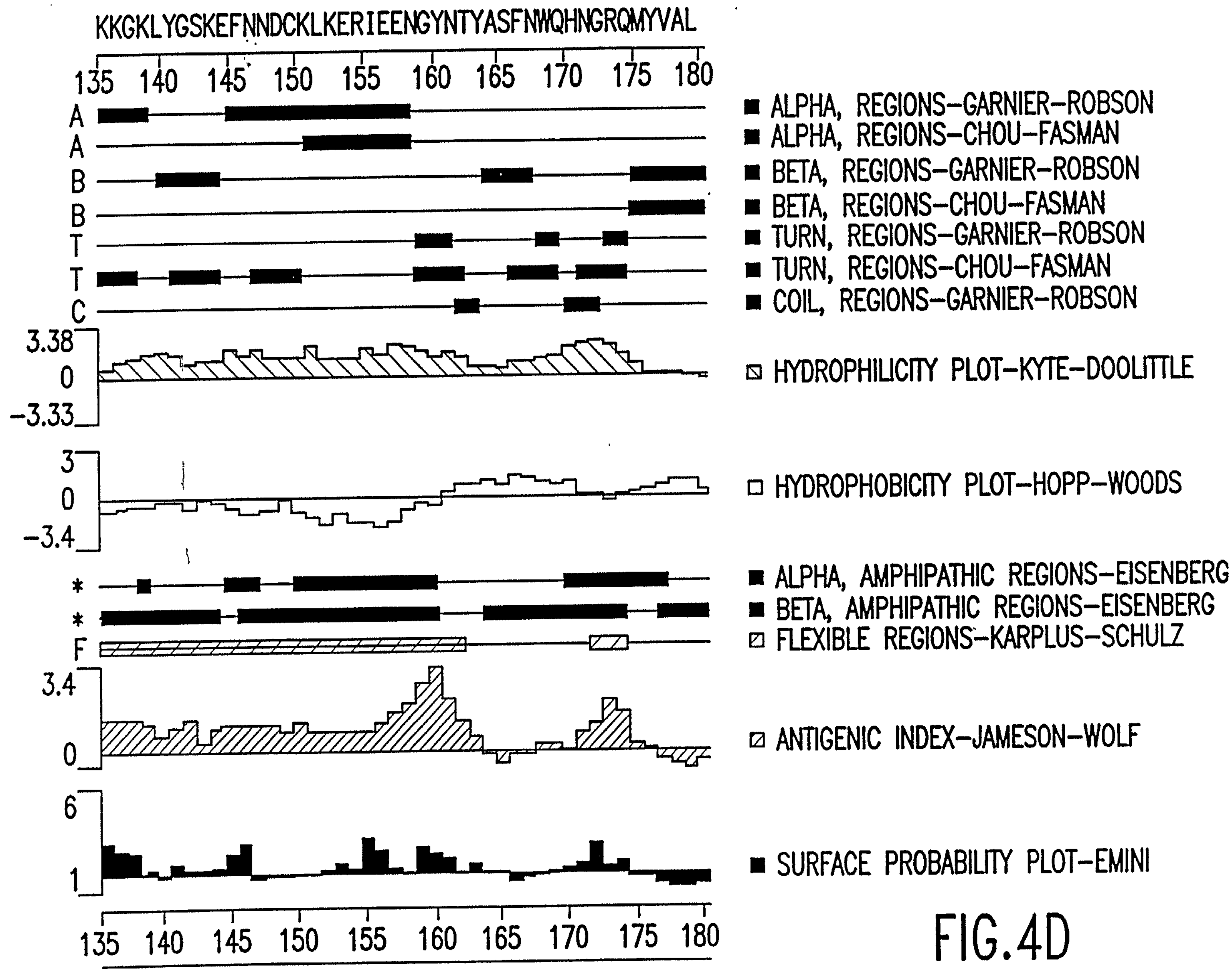
A
A
B
B
T
T
C
3.38
0
-3.33
3
0
-3.4
*
*
F
3.4
0
6
1
■ ALPHA, REGIONS-GARNIER-ROBSON
■ ALPHA, REGIONS-CHOU-FASMAN
■ BETA, REGIONS-GARNIER-ROBSON
■ BETA, REGIONS-CHOU-FASMAN
■ TURN, REGIONS-GARNIER-ROBSON
■ TURN, REGIONS-CHOU-FASMAN
■ COIL, REGIONS-GARNIER-ROBSON
□ HYDROPHILICITY PLOT-KYTE-DOOLITTLE
□ HYDROPHOBICITY PLOT-HOPP-WOODS
■ ALPHA, AMPHIPATHIC REGIONS-EISENBERG
■ BETA, AMPHIPATHIC REGIONS-EISENBERG
□ FLEXIBLE REGIONS-KARPLUS-SCHULZ
▨ ANTIGENIC INDEX-JAMESON-WOLF
■ SURFACE PROBABILITY PLOT-EMINI

FIG.4C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135 140 145 150 155 160 165 170 175 180
A
A
B
B
T
T
C
3.38
0
-3.33
3
0
-3.4
*
*
F
3.4
0
6
1
■ ALPHA, REGIONS-GARNIER-ROBSON
■ ALPHA, REGIONS-CHOU-FASMAN
■ BETA, REGIONS-GARNIER-ROBSON
■ BETA, REGIONS-CHOU-FASMAN
■ TURN, REGIONS-GARNIER-ROBSON
■ TURN, REGIONS-CHOU-FASMAN
■ COIL, REGIONS-GARNIER-ROBSON
▨ HYDROPHILICITY PLOT-KYTE-DOOLITTLE
□ HYDROPHOBICITY PLOT-HOPP-WOODS
■ ALPHA, AMPHIPATHIC REGIONS-EISENBERG
■ BETA, AMPHIPATHIC REGIONS-EISENBERG
▨ FLEXIBLE REGIONS-KARPLUS-SCHULZ
▨ ANTIGENIC INDEX-JAMESON-WOLF
■ SURFACE PROBABILITY PLOT-EMINI

FIG.4D

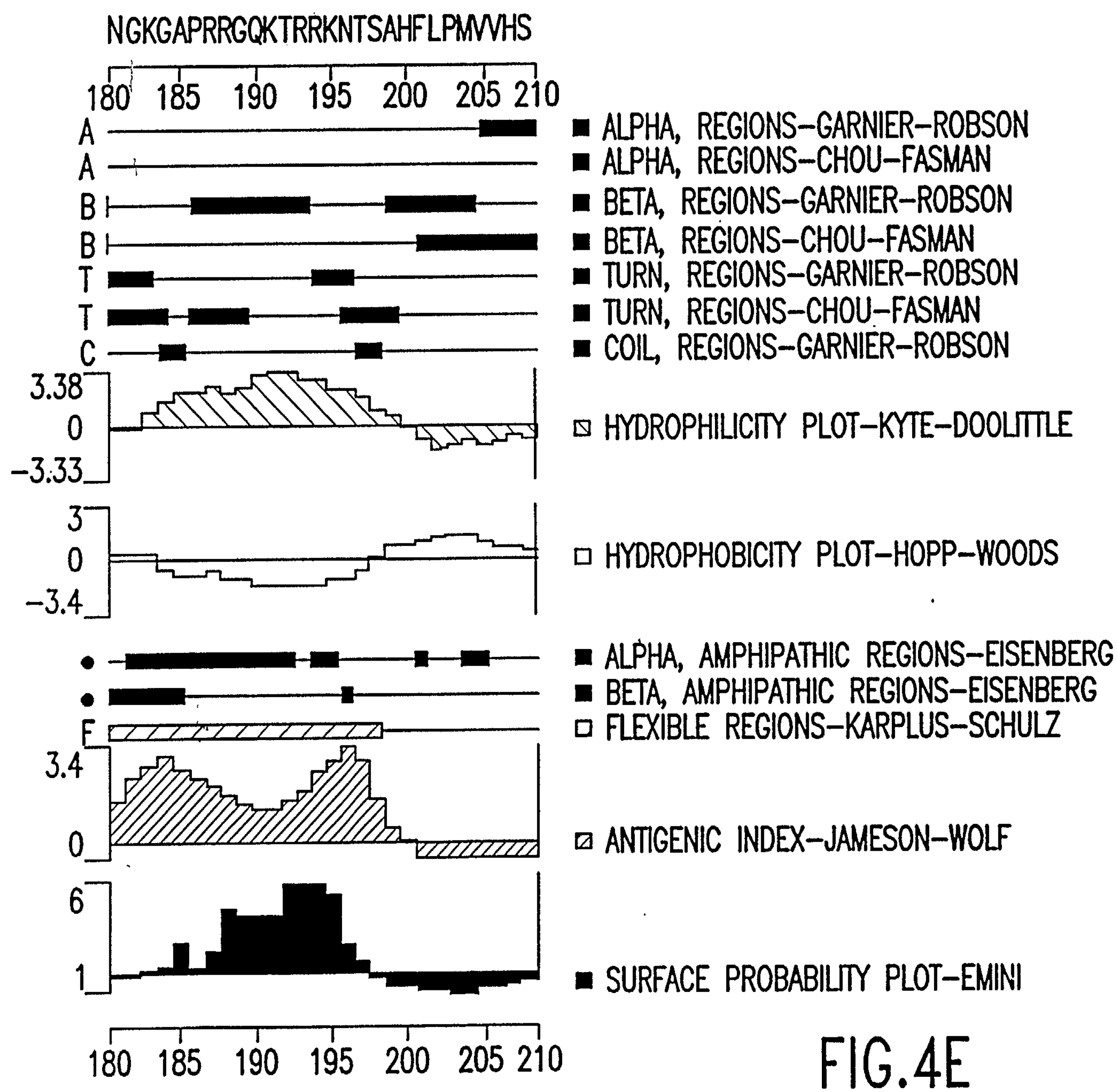
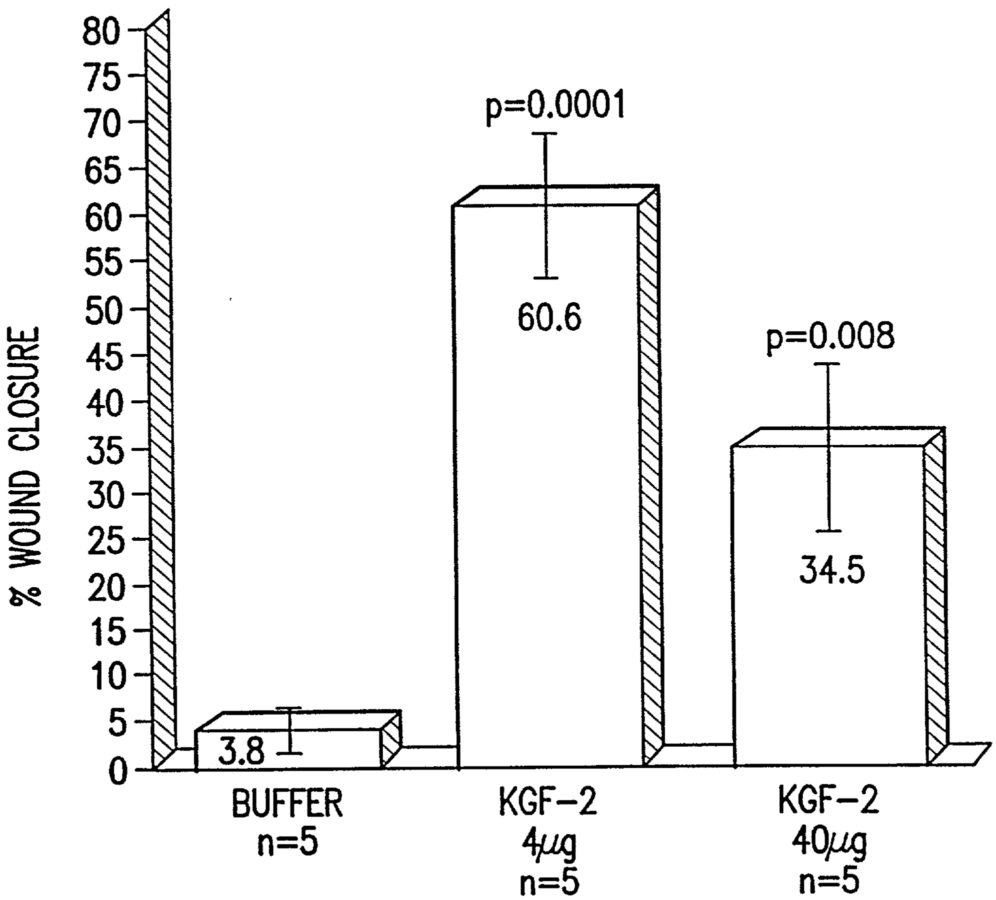
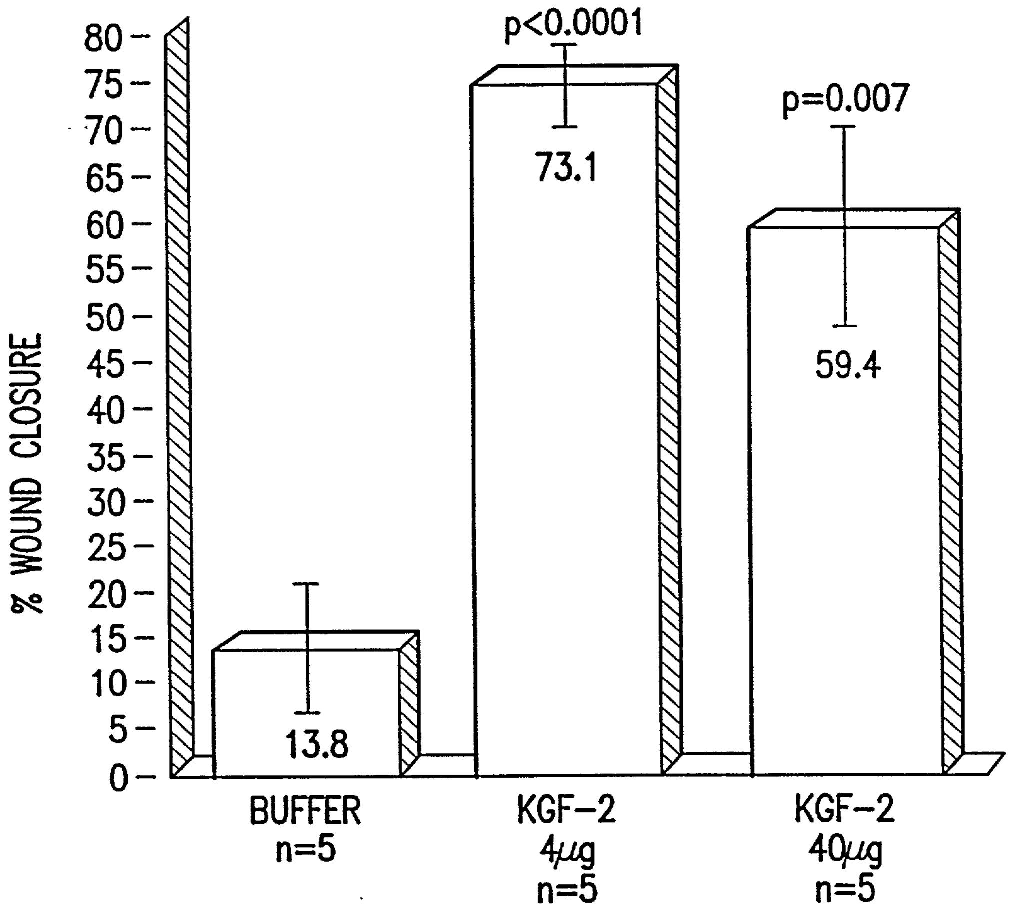

NGKGAPRRGQKTRRKNTSAHFLPMVVHS
180 185 190 195 200 205 210
A
A
B
B
T
T
C
ALPHA, REGIONS–GARNIER–ROBSON
ALPHA, REGIONS–CHOU–FASMAN
BETA, REGIONS–GARNIER–ROBSON
BETA, REGIONS–CHOU–FASMAN
TURN, REGIONS–GARNIER–ROBSON
TURN, REGIONS–CHOU–FASMAN
COIL, REGIONS–GARNIER–ROBSON
3.38
0
–3.33
HYDROPHILICITY PLOT–KYTE–DOOLITTLE
3
0
–3.4
HYDROPHOBICITY PLOT–HOPP–WOODS
ALPHA, AMPHIPATHIC REGIONS–EISENBERG
BETA, AMPHIPATHIC REGIONS–EISENBERG
F
FLEXIBLE REGIONS–KARPLUS–SCHULZ
3.4
0
ANTIGENIC INDEX–JAMESON–WOLF
6
1
SURFACE PROBABILITY PLOT–EMINI
180 185 190 195 200 205 210

FIG.4E



80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
% WOUND CLOSURE
p=0.0001
60.6
p=0.008
34.5
3.8
BUFFER
n=5
KGF-2
4μg
n=5
KGF-2
40μg
n=5

FIG.5



% WOUND CLOSURE
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
p<0.0001
p=0.007
13.8
73.1
59.4
BUFFER
n=5
KGF-2
4μg
n=5
KGF-2
40μg
n=5

FIG.6

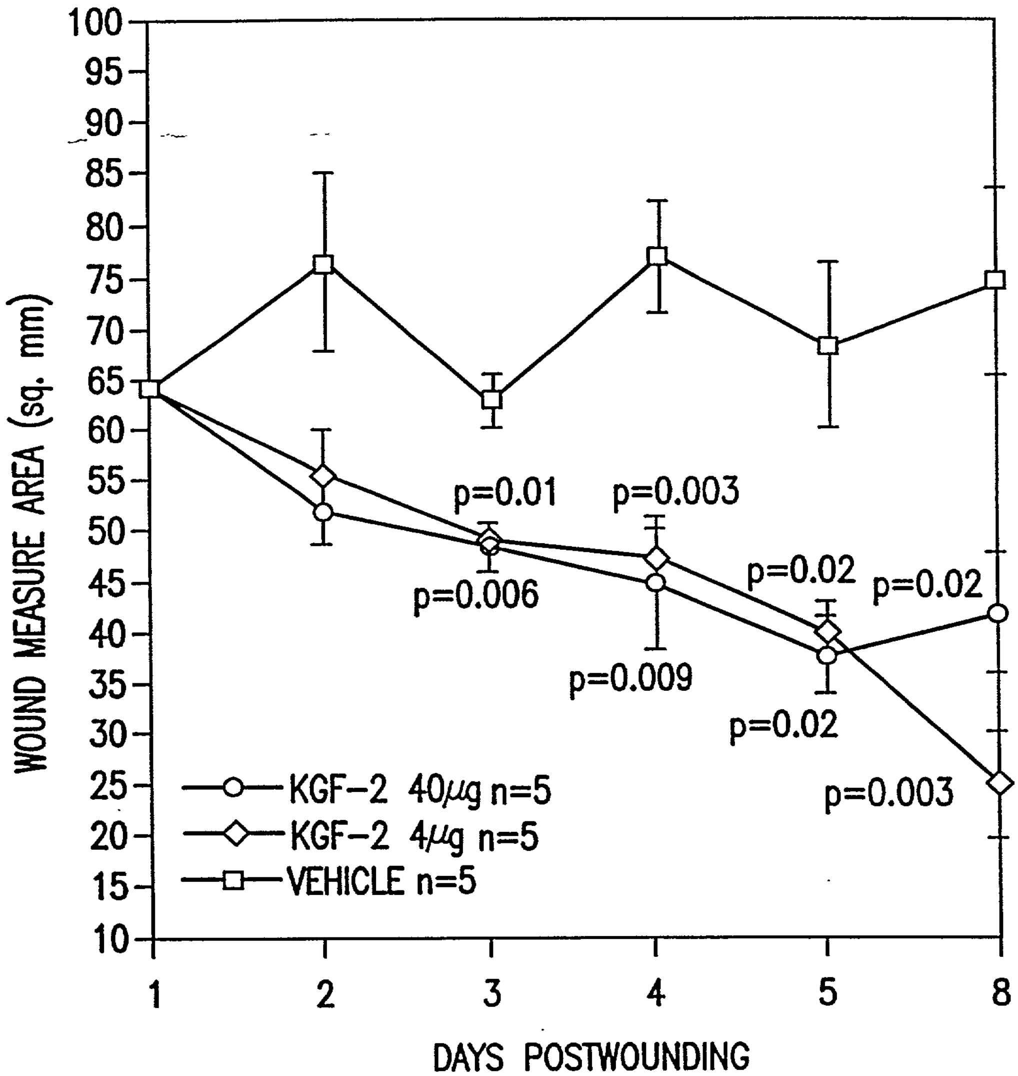

100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
WOUND MEASURE AREA (sq. mm)
1
2
3
4
5
8
DAYS POSTWOUNDING
p=0.01
p=0.003
p=0.006
p=0.02
p=0.02
p=0.009
p=0.02
p=0.003
KGF-2 40μg n=5
KGF-2 4μg n=5
VEHICLE n=5

FIG.7

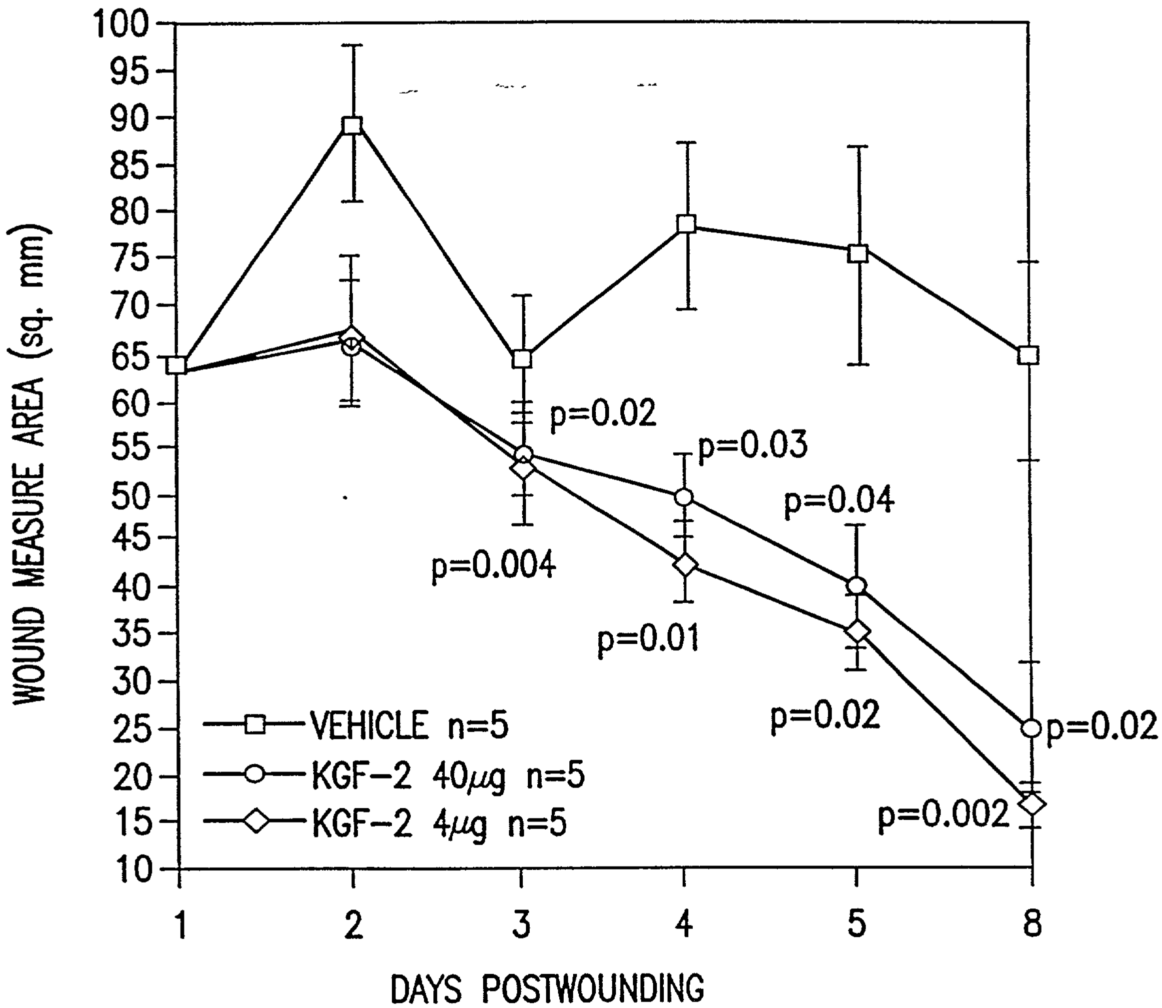
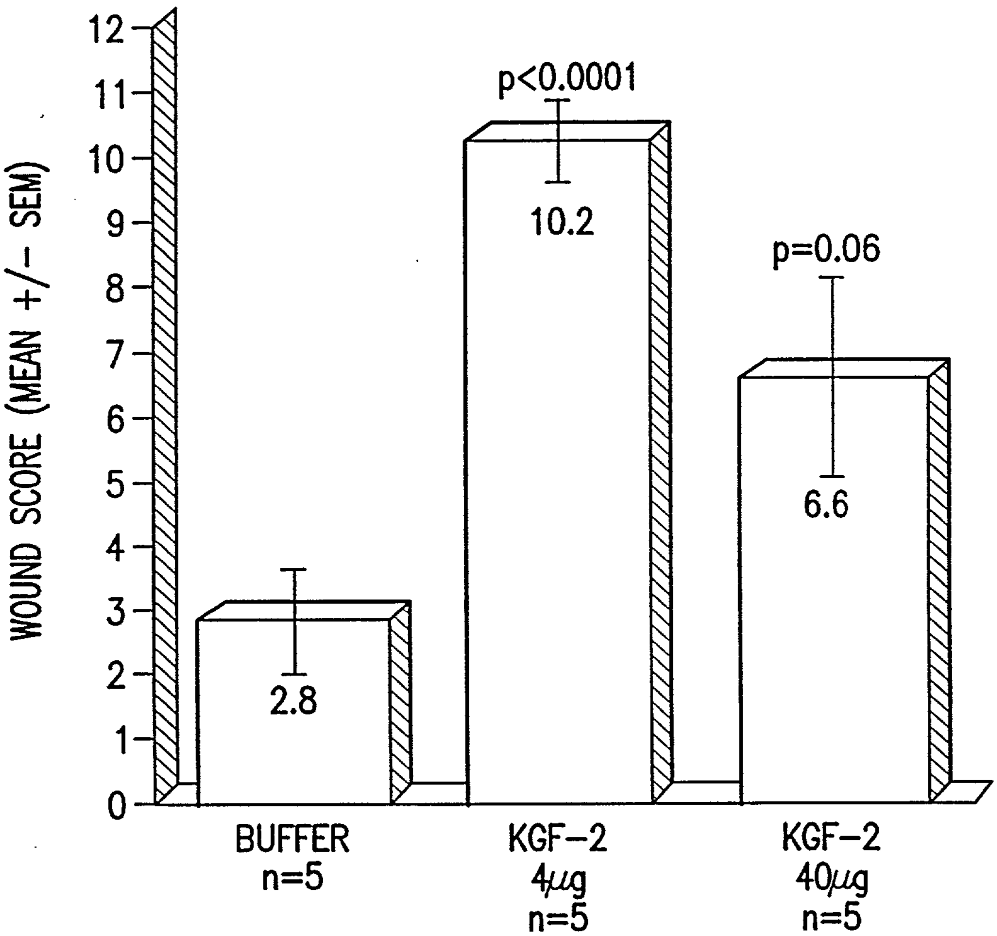
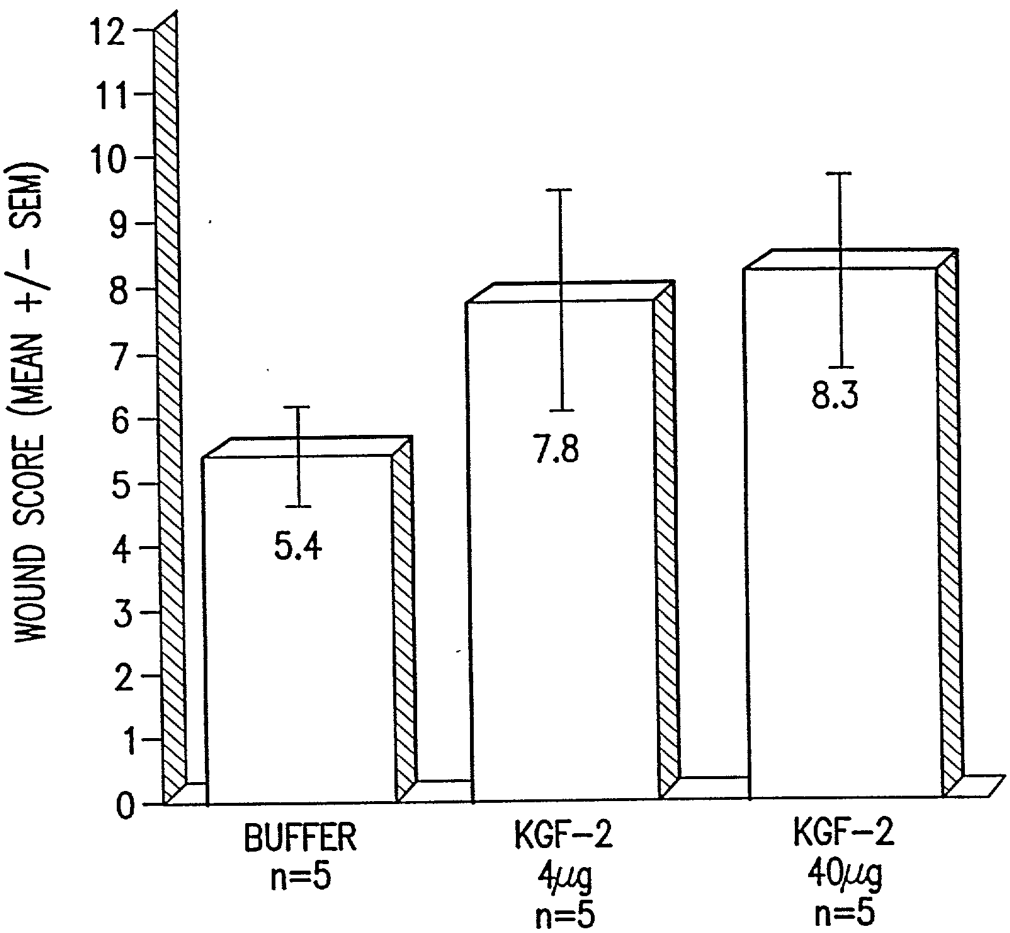

WOUND MEASURE AREA (sq. mm)
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
1
2
3
4
5
8
DAYS POSTWOUNDING
p=0.02
p=0.03
p=0.04
p=0.004
p=0.01
p=0.02
p=0.02
p=0.002
VEHICLE n=5
KGF-2 40μg n=5
KGF-2 4μg n=5

FIG.8



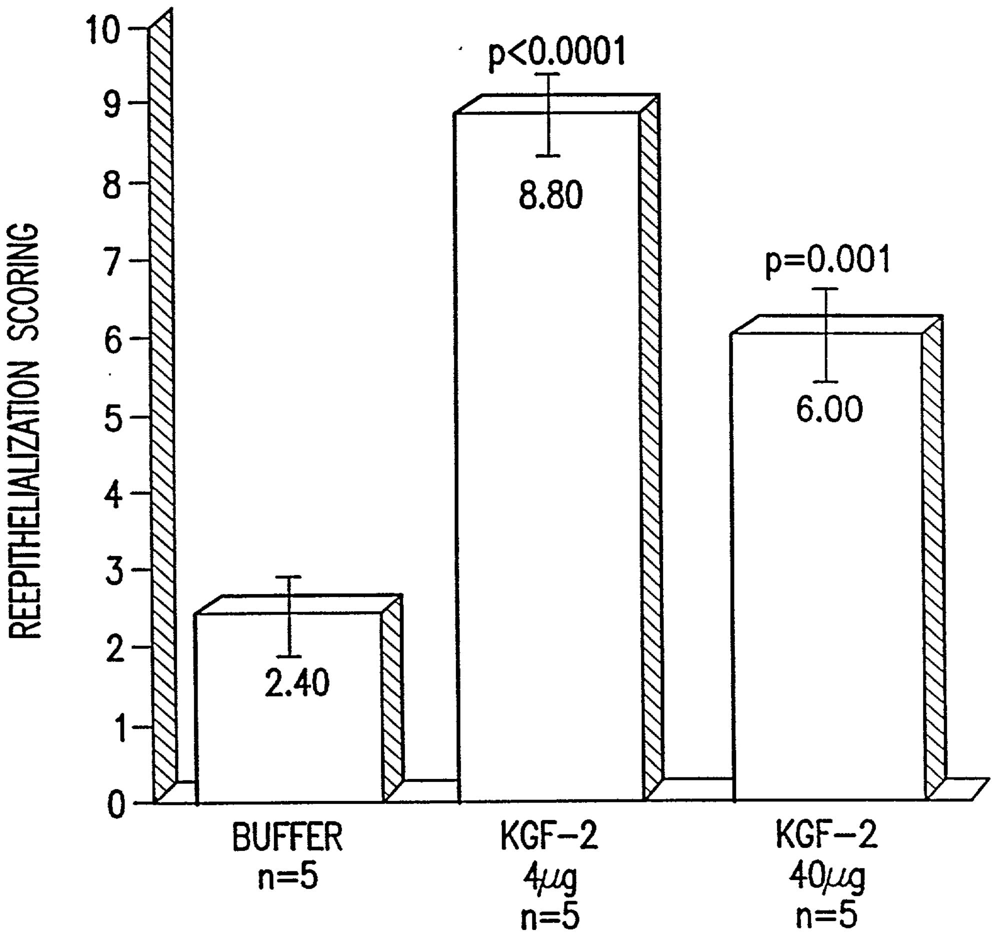
1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.9



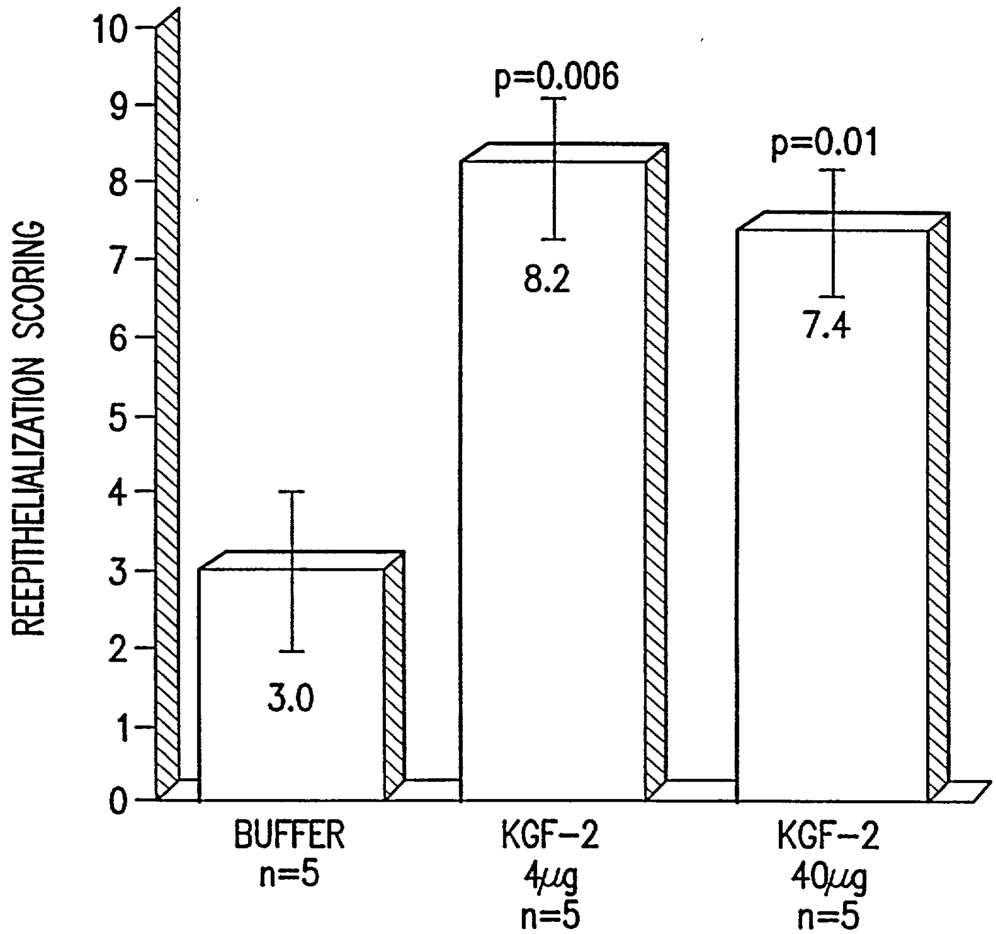
1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES
7-9 GRANULATION TISSUE, CELLS, FIBROBLASTS, NEW EPITHELIUM
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.10



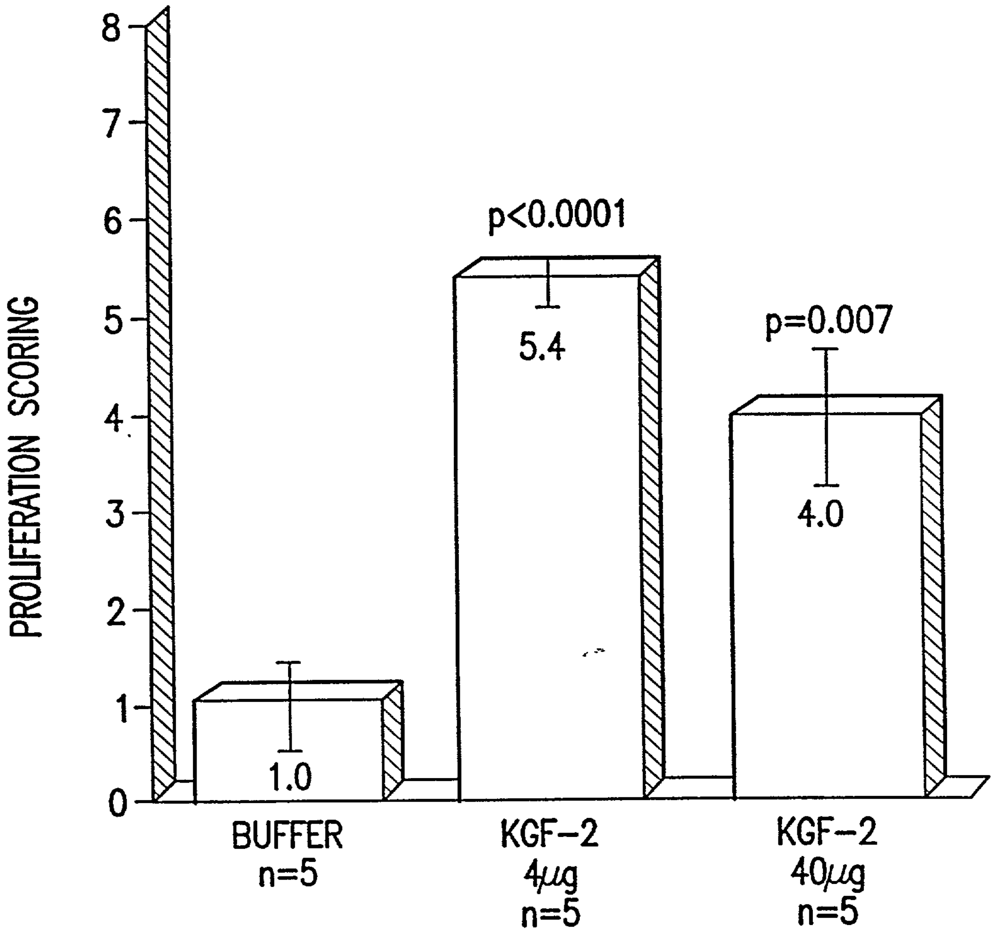
ANTI-CYTOKERATIN IMMUNOSTAINING
0-NO CLOSURE
5-SLIGHT TO MODERATE CLOSURE
10-COMPLETE CLOSURE

FIG.11



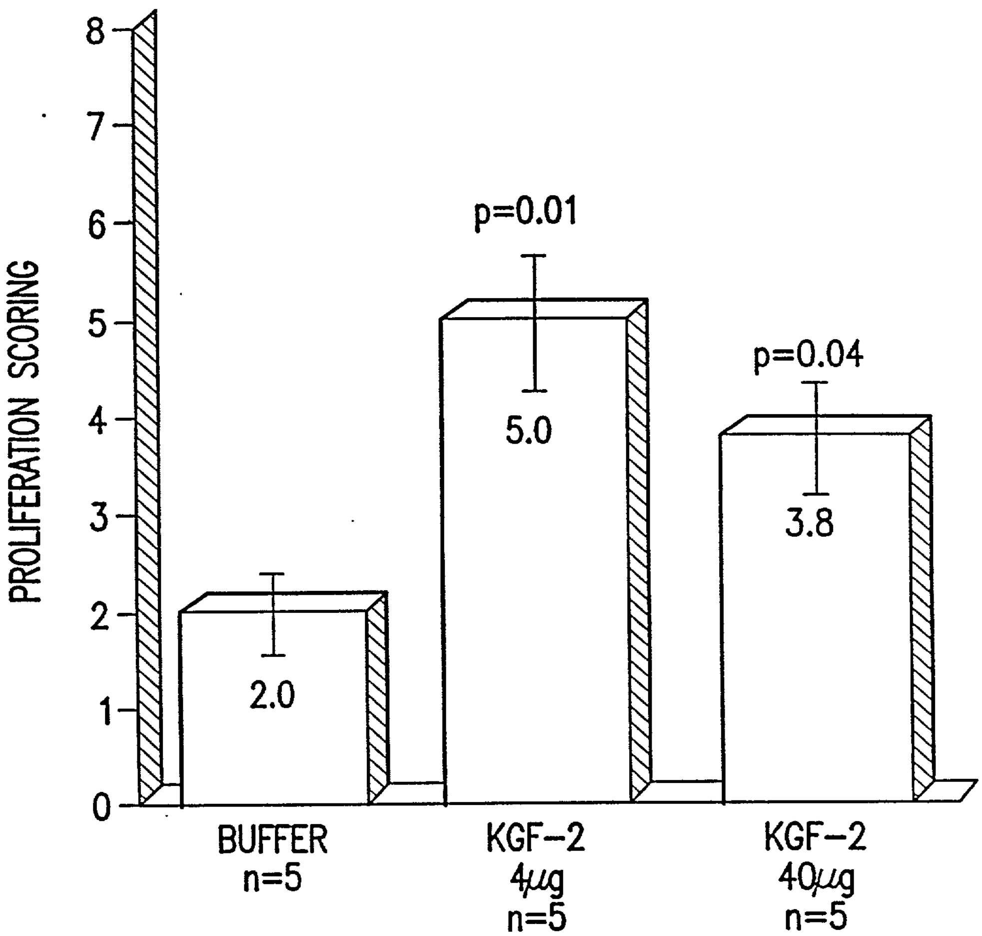
ANTI-CYTOKERATIN IMMUNOSTAINING
0-NO CLOSURE
5-SLIGHT TO MODERATE CLOSURE
10-COMPLETE CLOSURE

FIG.12



PCNA SCORING
0–2 SLIGHT PROLIFERATION
3–5 MODERATE PROLIFERATION
6–8 INTENSE PROLIFERATION

FIG.13



PCNA SCORING
0–2 SLIGHT PROLIFERATION
3–5 MODERATE PROLIFERATION
6–8 INTENSE PROLIFERATION

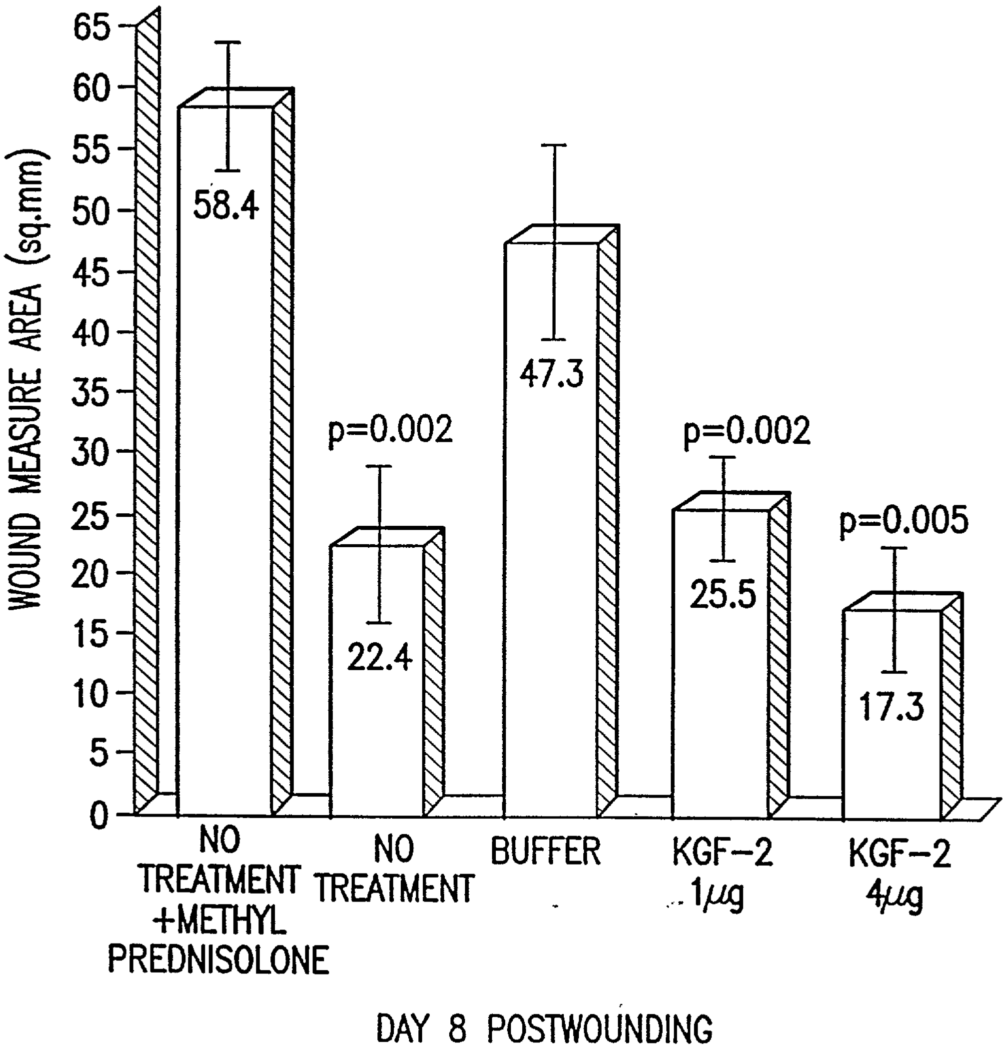
FIG.14

ATGAGAGGATCGCATCACCATCACCATCACGGATCCTGCCAGGCTCTGGGTC
AGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTTCTCTTCCC
CGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTC
GTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTG
GAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAG
CAACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAG
AATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGAT
ACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT
GTGGCATTGAaTGGAAAAGGAGCTCCAaGGAGAGGACAGAAAACACGAAG
GAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MRGSHHHHHHGSCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGD
VRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSN
YYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS

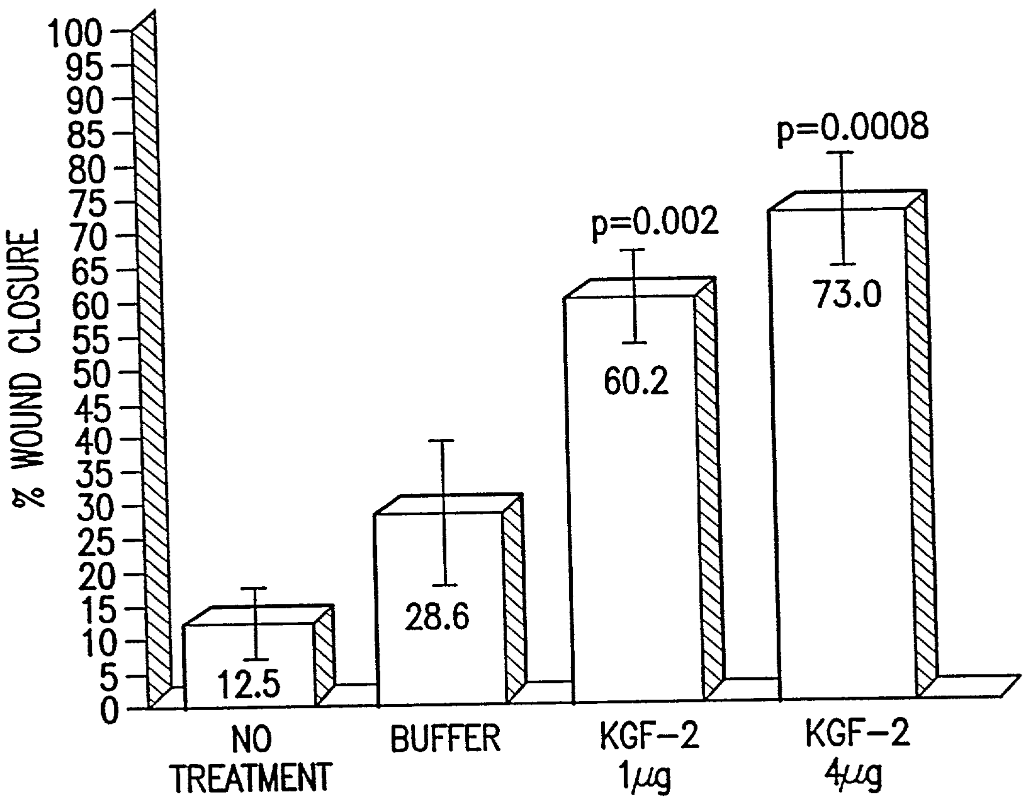
kgf-2 synthetic cys37 Bam HI
AAAGGATCCTGCCAGGCTCTGGGTCAGGACATG

FIG.15



WOUND MEASURE AREA (sq.mm)
65
60
55
50
45
40
35
30
25
20
15
10
5
0
58.4
p=0.002
22.4
47.3
p=0.002
25.5
p=0.005
17.3
NO TREATMENT +METHYL PREDNISOLONE
NO TREATMENT
BUFFER
KGF-2 1μg
KGF-2 4μg
DAY 8 POSTWOUNDING

FIG.16



GLUCOCORTICOID TREATED ANIMALS

FIG.17

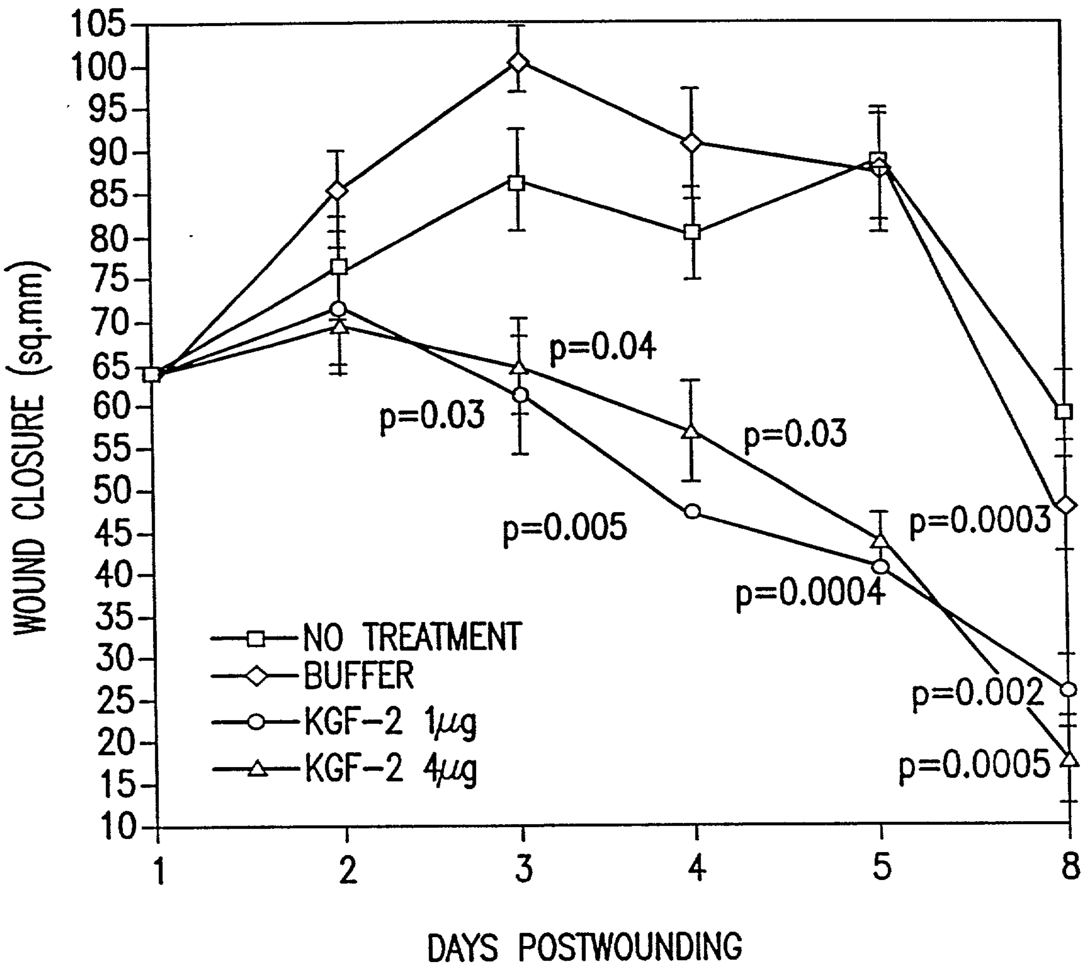

WOUND CLOSURE (sq.mm)
105
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
1
2
3
4
5
8
DAYS POSTWOUNDING
NO TREATMENT
BUFFER
KGF-2 1μg
KGF-2 4μg
p=0.04
p=0.03
p=0.03
p=0.005
p=0.0003
p=0.0004
p=0.002
p=0.0005

FIG.18

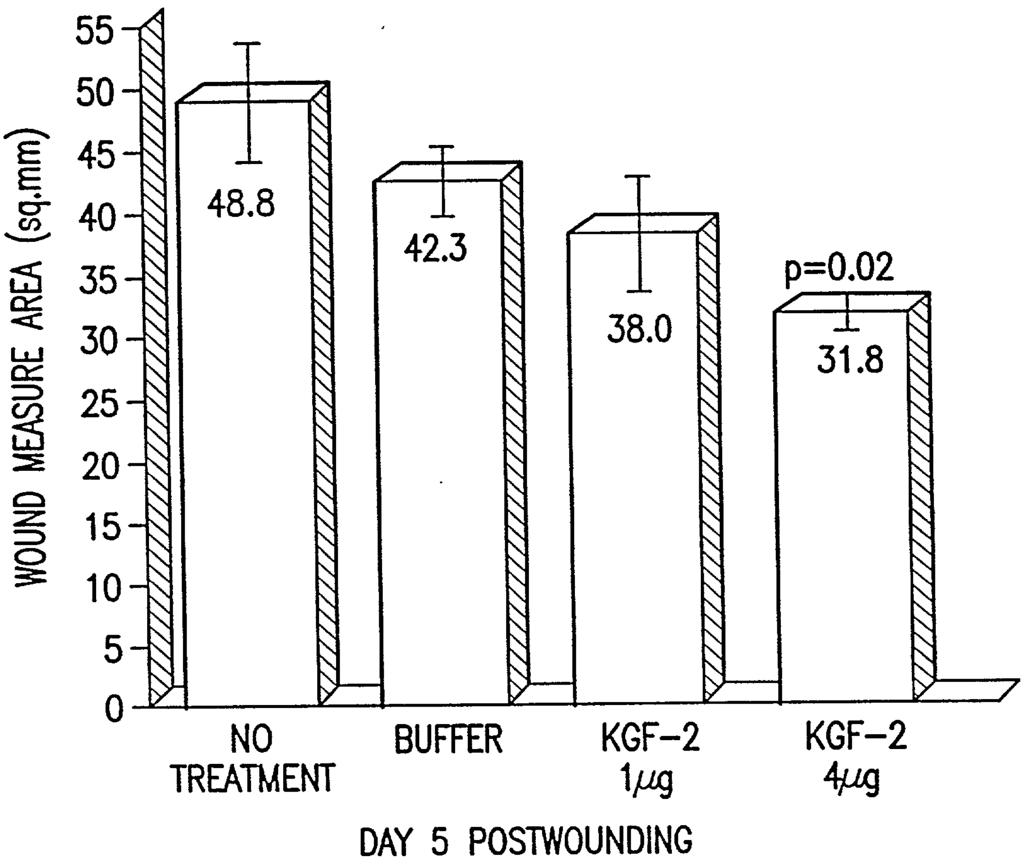

WOUND MEASURE AREA (sq.mm)
55
50
45
40
35
30
25
20
15
10
5
0
48.8
42.3
38.0
p=0.02
31.8
NO TREATMENT
BUFFER
KGF-2 1μg
KGF-2 4μg
DAY 5 POSTWOUNDING

FIG.19A

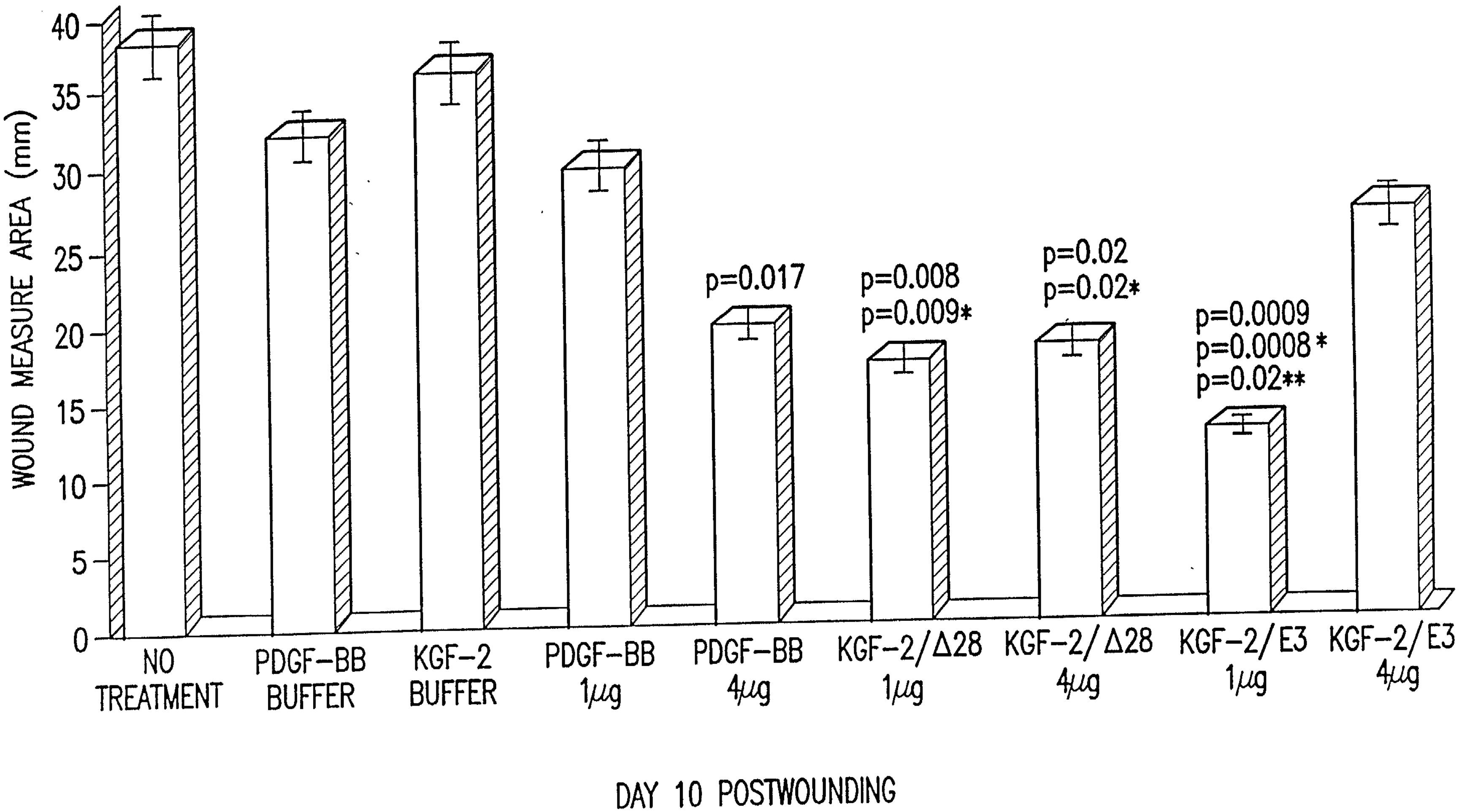

WOUND MEASURE AREA (mm)
0
5
10
15
20
25
30
35
40
p=0.017
p=0.008
p=0.009*
p=0.02
p=0.02*
p=0.0009
p=0.0008 *
p=0.02**
NO TREATMENT
PDGF-BB BUFFER
KGF-2 BUFFER
PDGF-BB 1μg
PDGF-BB 4μg
KGF-2/Δ28 1μg
KGF-2/Δ28 4μg
KGF-2/E3 1μg
KGF-2/E3 4μg
DAY 10 POSTWOUNDING

FIG.19B

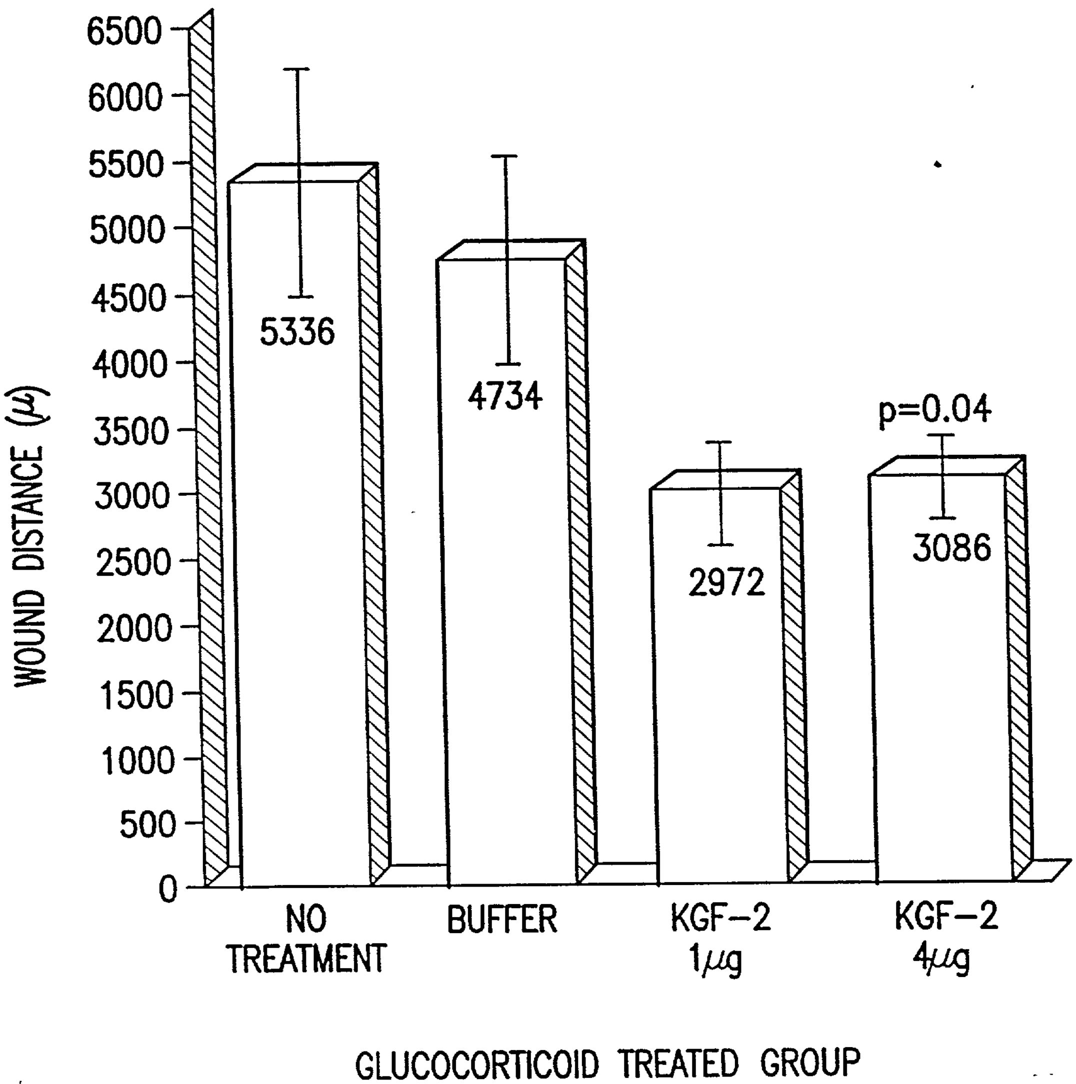

WOUND DISTANCE (μ)
6500
6000
5500
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
5336
4734
2972
3086
p=0.04
NO TREATMENT
BUFFER
KGF-2 1μg
KGF-2 4μg
GLUCOCORTICOID TREATED GROUP

FIG.20

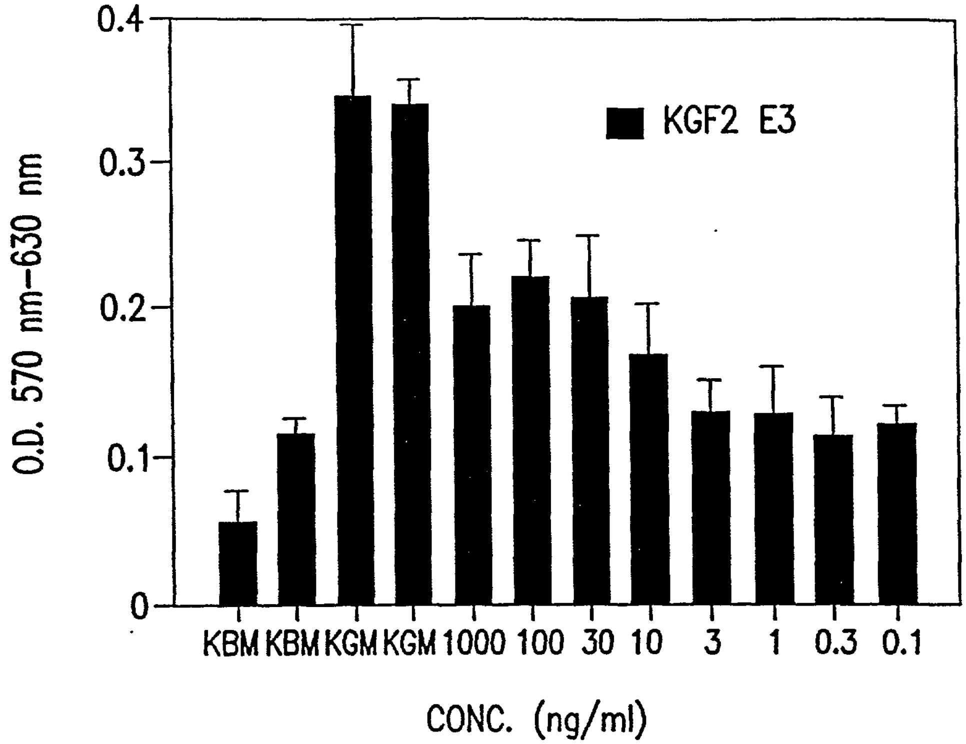


FIG.21A

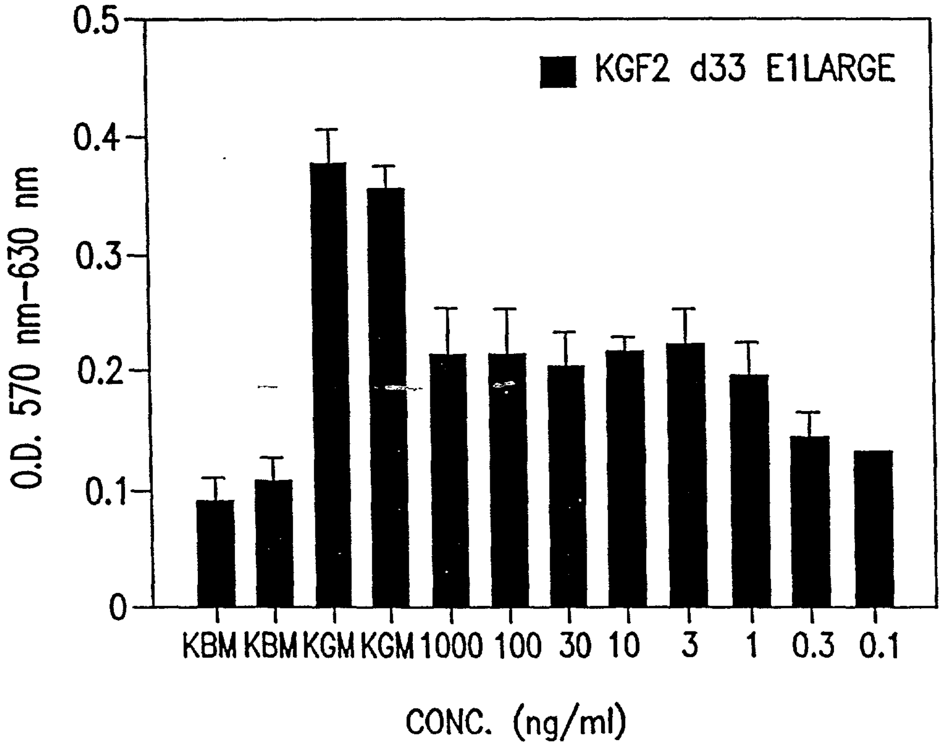


FIG.21B

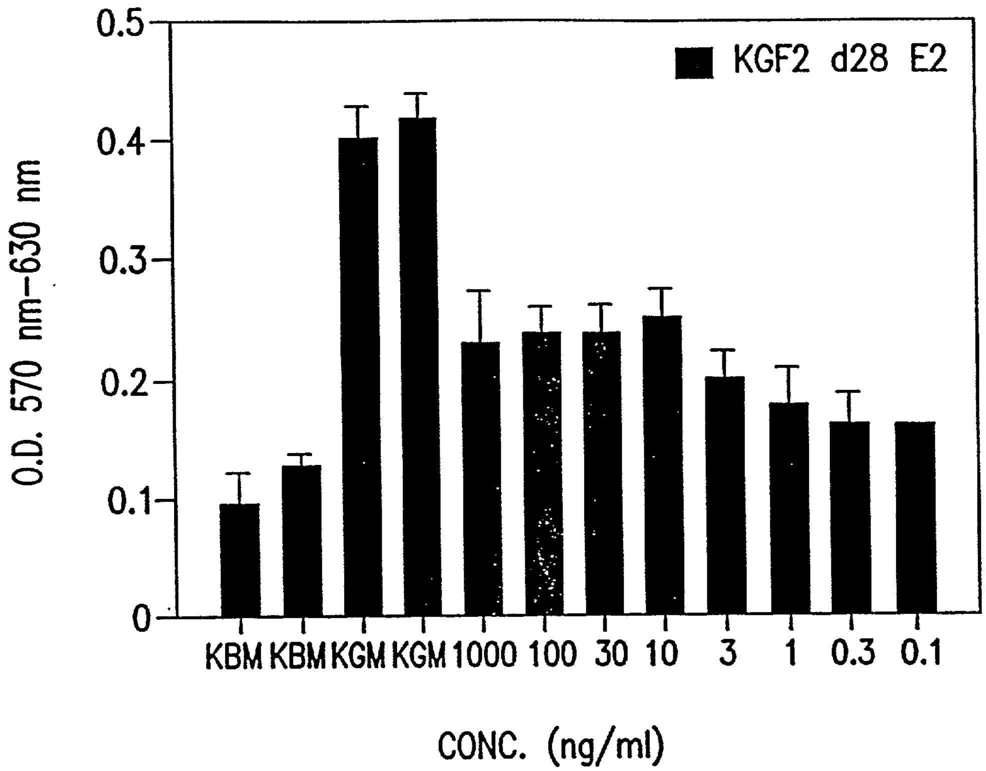


FIG.21C

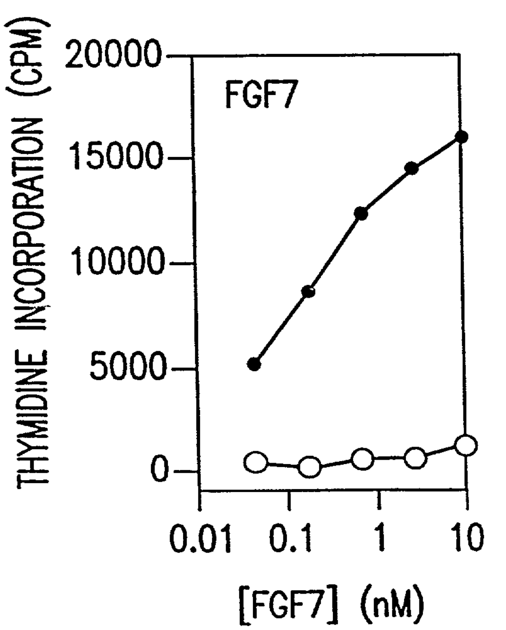


FIG.22A

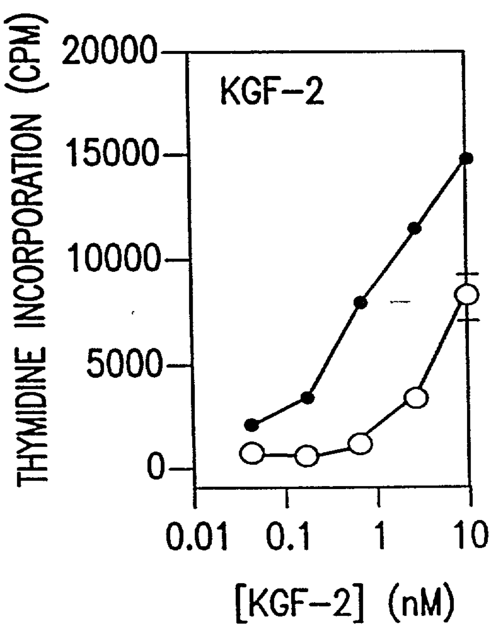


FIG.22A–1

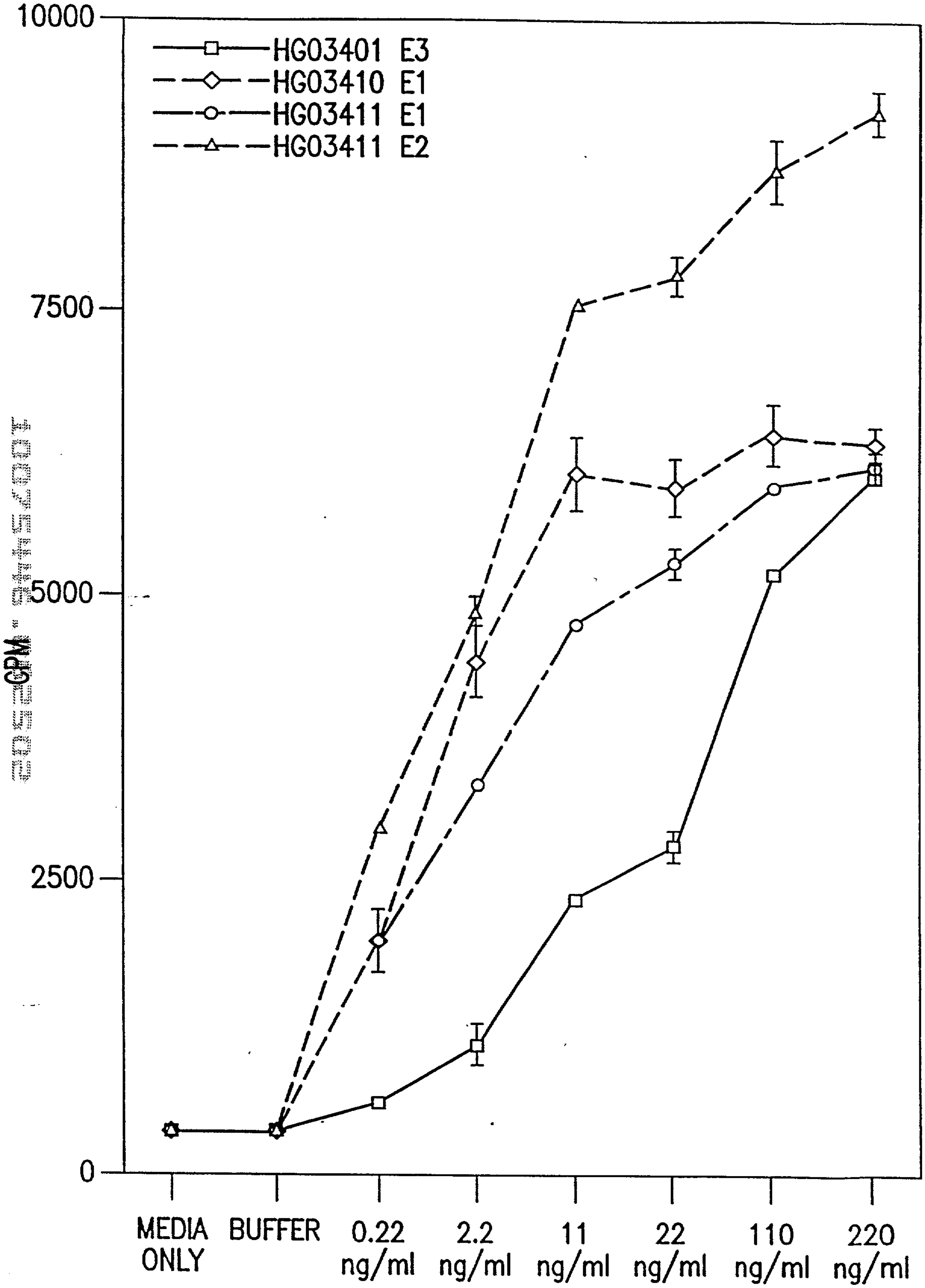

10000
7500
5000
2500
0
CPM
HG03401 E3
HG03410 E1
HG03411 E1
HG03411 E2
MEDIA ONLY
BUFFER
0.22 ng/ml
2.2 ng/ml
11 ng/ml
22 ng/ml
110 ng/ml
220 ng/ml

FIG.22B

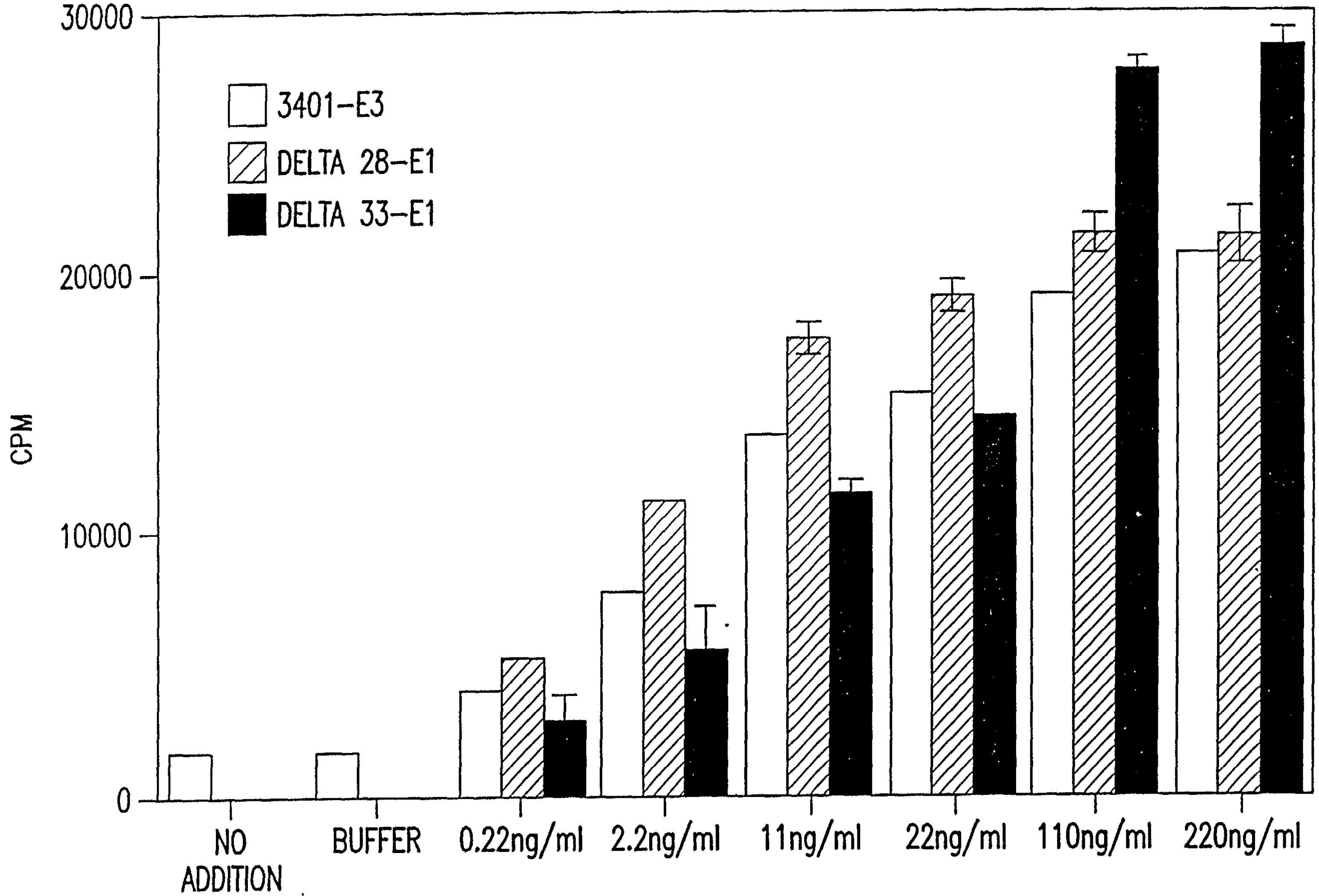

30000
20000
10000
0
CPM
3401-E3
DELTA 28-E1
DELTA 33-E1
NO ADDITION
BUFFER
0.22ng/ml
2.2ng/ml
11ng/ml
22ng/ml
110ng/ml
220ng/ml

FIG.22C

ATGTGGAAATGGATACTGACCCACTGCGCTTCTGCTTTCCCGCACCTGCCGGGTTGCTGC 60
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro Gly Cys Cys

TGCTGCTGCTTCCTGCTGCTGTTCCTGGTTTCTTCTGTTCCGGTTACCTGCCAGGCTCTG 120
Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val Pro Val Thr Cys Gln Ala Leu

GGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTTCTCTTCCCCG 180
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro

ACTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTCGTTGGCGT 240
Thr Ser Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg

AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCTGGG 300
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly

ACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT 360
Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val

GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC 420
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu

TATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA 480
Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly

TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG 540
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu

AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC 600
Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His

TTTCTTCCAATGGTGGTACACTCATAG 627
Phe Leu Pro Met Val Val His Ser *

FIG.23

```
ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCT    60
MetThrCysGlnAlaLeuGlyGlnAspMetValSerProGluAlaThrAsnSerSerSer

TCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAG   120
SerSerPheSerSerProSerSerAlaGlyArgHisValArgSerTyrAsnHisLeuGln

GGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA   180
GlyAspValArgTrpArgLysLeuPheSerPheThrLysTyrPheLeuLysIleGluLys

AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACA   240
AsnGlyLysValSerGlyThrLysLysGluAsnCysProTyrSerIleLeuGluIleThr

TCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATG   300
SerValGluIleGlyValValAlaValLysAlaIleAsnSerAsnTyrTyrLeuAlaMet

AACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAG   360
AsnLysLysGlyLysLeuTyrGlySerLysGluPheAsnAsnAspCysLysLeuLysGlu

AGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG   420
ArgIleGluGluAsnGlyTyrAsnThrTyrAlaSerPheAsnTrpGlnHisAsnGlyArg

CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG   480
GlnMetTyrValAlaLeuAsnGlyLysGlyAlaProArgArgGlyGlnLysThrArgArg

AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG   525
LysAsnThrSerAlaHisPheLeuProMetValValHisSer *
```

FIG.24A

ATGACTTGCCAGGCACTGGGTCAAGACATGGTTTCCCCGGAAGCTACCAACAGCTCCAGCTCTAGCTTCA 70

TACTGAACGGTCCGTGACCCAGTTCTGTACCAAAGGGGCCTTCGATGGTTGTCGAGGTCGAGATCGAAGT

M T C Q A L G Q D M V S P E A T N S S S S S F

GCAGCCCATCTAGCGCAGGTCGTCACGTTCGCTCTTACAACCACTTACAGGGTGATGTTCGTTGGCGCAA 140

CGTCGGGTAGATCGCGTCCAGCAGTGCAAGCGAGAATGTTGGTGAATGTCCCACTACAAGCAACCGCGTT

S S P S S A G R H V R S Y N H L Q G D V R W R K

ACTGTTCAGCTTTACCAAGTACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAG 210

TGACAAGTCGAAATGGTTCATGAAGGACTTTTAGCTTTTTTTGCCATTTCAAAGACCCTGGTTCTTCCTC

L F S F T K Y F L K I E K N G K V S G T K K E

AACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACA 280

TTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAACAACGGCAGTTTCGGTAATTGT

N C P Y S I L E I T S V E I G V V A V K A I N

GCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAA 350

CGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAGATACCGAGTTTTCTTAAATTGTTACTGACATT

S N Y Y L A M N K K G K L Y G S K E F N N D C K

GCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG 420

CGACTTCCTCTCCTATCTCCTTTTACCTATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCC

L K E R I E E N G Y N T Y A S F N W Q H N G R

CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCT 490

GTTTACATACACCGTAACTTACCTTTTCCTCGAGGTTCCTCTCCTGTCTTTTGTGCTTCCTTTTTGTGGA

Q M Y V A L N G K G A P R R G Q K T R R K N T

CTGCTCACTTTCTTCCAATGGTGGTACACTCATAG 525

GACGAGTGAAAGAAGGTTACCACCATGTGAGTATC

S A H F L P M V V H S

FIG.24B

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCAC
CTGCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIE
KNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDCKL
KERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.25

ATGGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTCGTTGGCGT
AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG
GGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATA
GAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAA
ATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG
AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGV
VAVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.26

ATGGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATA
ACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTA
GCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAG
CTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAG
CATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGA
CAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCA
TAG

MVRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAM
NKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTR
RKNTSAHFLPMVVHS.

FIG.27

ATGGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCAT
CCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCA
ACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAAC
AATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATC
ATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAG
CTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCA
ATGGTGGTACACTCATAG

MEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDC
KLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVH
S.

FIG.28

ATGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGT
TGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAAC
TCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAA
AATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTA
TGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAA
ACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGY
NTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.29

ATGGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACT
CTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAA
ATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT
GTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAA
CACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.30

ATGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAG
GATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGA
GGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACA
CGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKT
RRKNTSAHFLPMVVHS.

FIG.31

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCAC
CTGCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAAT
GACTGTAAGCTGAAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIE
KNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDCKL
K

FIG.32

ATGGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTCGTTGGCGT
AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG
GGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAG

MAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGV
VAVKAINSNYYLAMNKKGKLYGSKEFNNDCKLK

FIG.33

C-37 To Ser

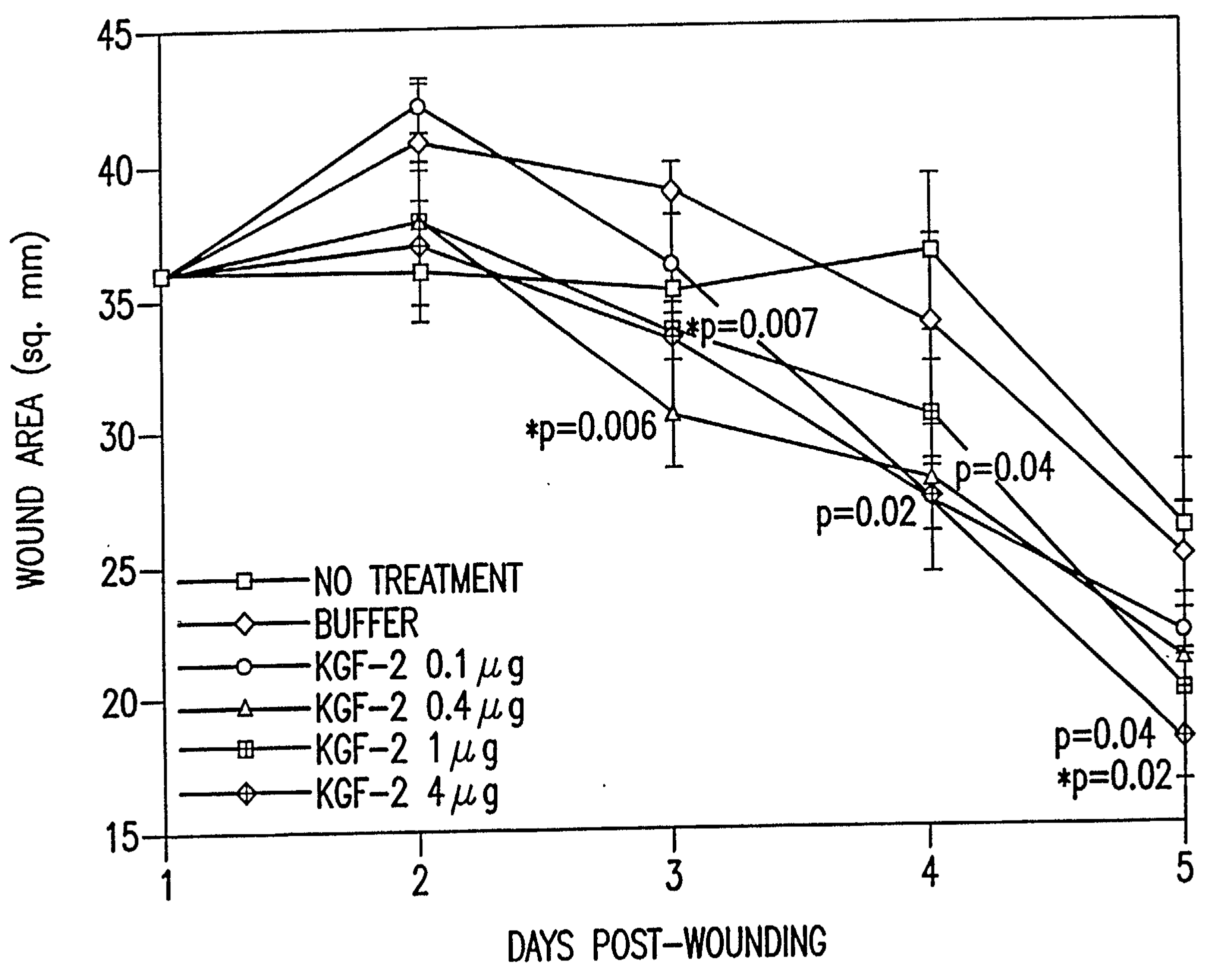
ATGACCTCTCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCAC
CTGCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

FIG.34

C-106 To Ser

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCAC
CTGCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTCTCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

FIG.35



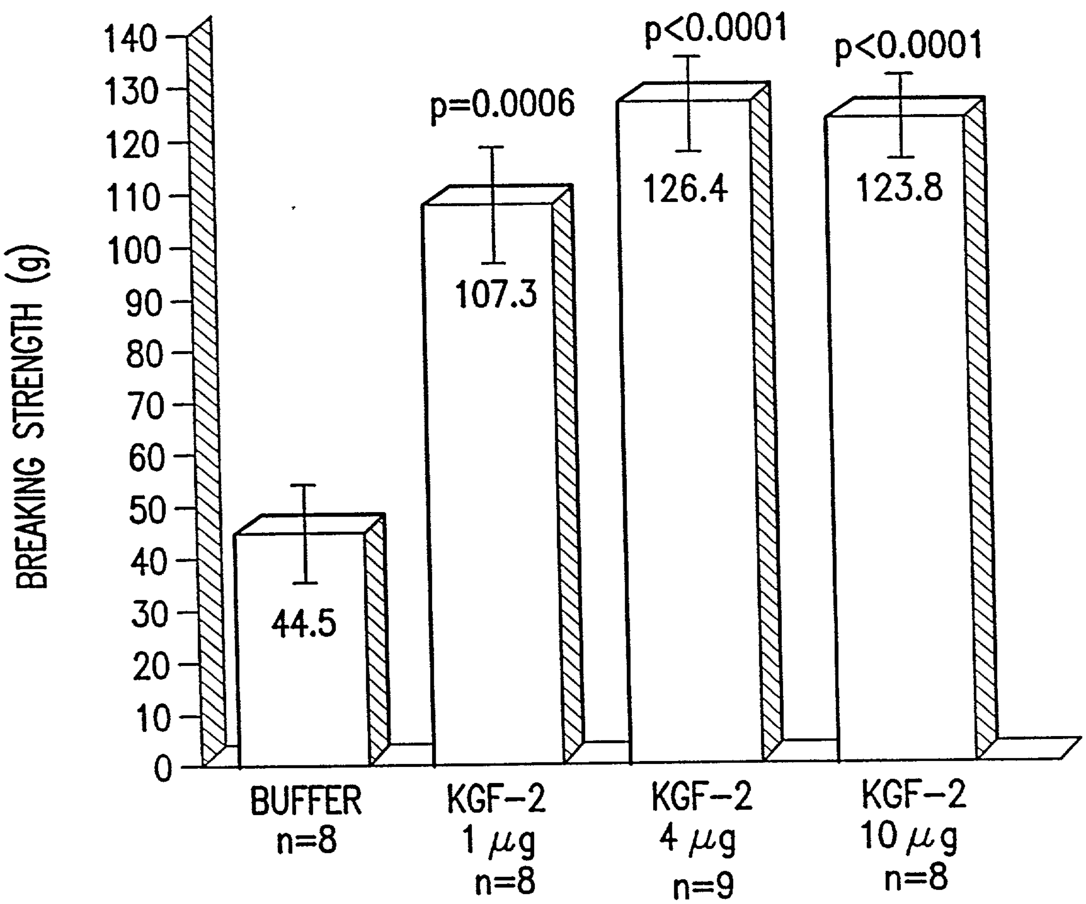
WOUND AREA (sq. mm)
45
40
35
30
25
20
15
1
2
3
4
5
DAYS POST-WOUNDING
NO TREATMENT
BUFFER
KGF-2 0.1 μg
KGF-2 0.4 μg
KGF-2 1 μg
KGF-2 4 μg
*p=0.007
*p=0.006
p=0.04
p=0.02
p=0.04
*p=0.02

FIG.36

EFFECT OF KGF-2 Δ33 ON NORMAL WOUND HEALING RAT MODEL

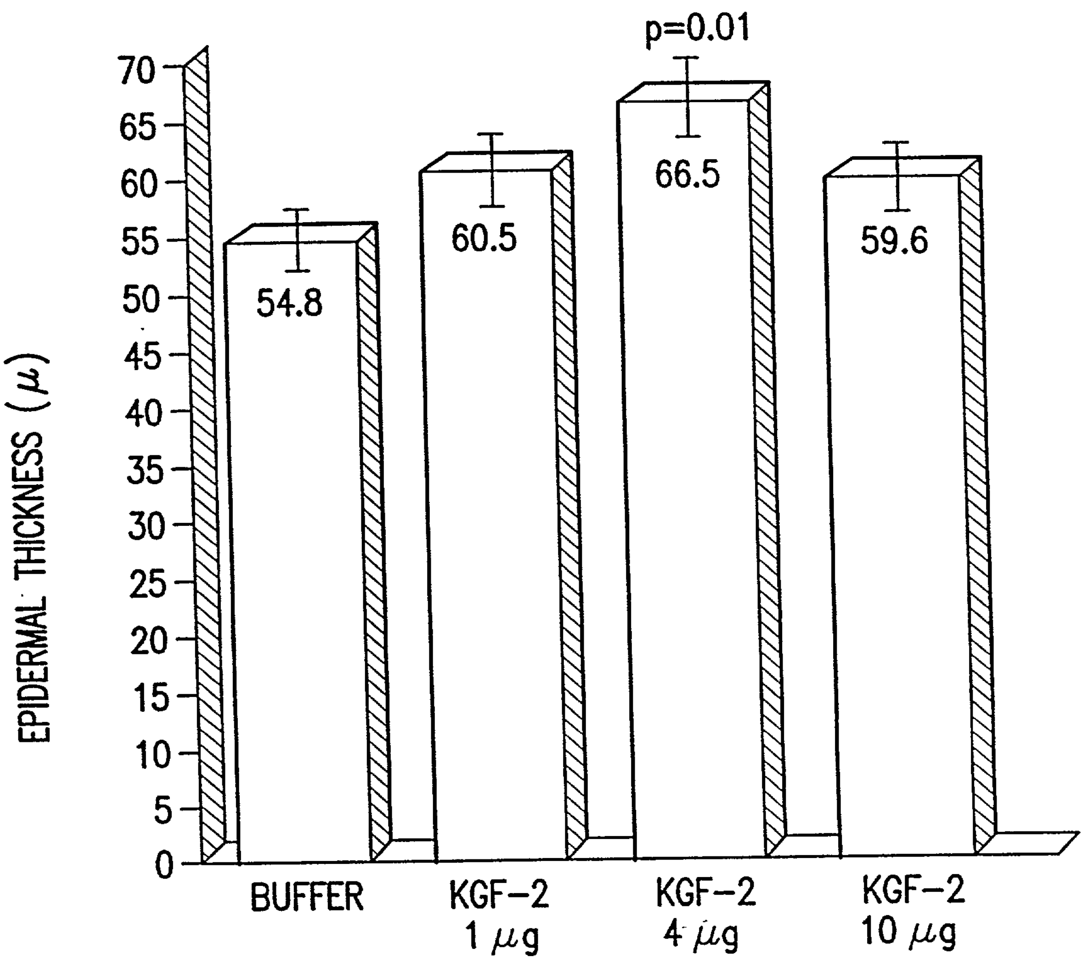
TREATMENT GROUPS	WOUND SIZE (mm)	% WOUND CLOSURE	HISTOLOGICAL SCORE	RE-EPITH. (μm)	BrdU SCORE
NO TREATMENT	25.9±2.5	58.8±3.7	6.8±0.2	1142±141	3.8±0.4
BUFFER	25.1±1.7	60.2±2.6	6.4±0.2	923±61	5.0±0.4
KGF-2/Δ33 (0.1μg)	22.0±0.9	65±1.4	6.8±0.2	1275±148	4.6±0.7
KGF-2/Δ33 (0.4μg)	21.1±1.4	68.4±2.4	8.0±0.5 p=0.0445*	1310±182	4.2±0.7
KGF-2/Δ33 (1.0μg)	19.9±1.5	66.2±2.1	8.4±0.4 p=0.0159* p=0.0053†	1389±115 p=0.0074†	3.3±0.25 p=0.0217†
KGF-2/Δ33 (4.0μg)	18.1±1.6 p=0.0398* p=0.0200†	71.2±2.6 p=0.0367* p=0.0217†	8.5±0.3 p=0.0047* p=0.0445†	1220±89 p=0.0254†	5.3±0.9

FIG.37



BREAKING STRENGTH (g)
140
130
120
110
100
90
80
70
60
50
40
30
20
10
0
44.5
p=0.0006
107.3
p<0.0001
126.4
p<0.0001
123.8
BUFFER
n=8
KGF-2
1 μg
n=8
KGF-2
4 μg
n=9
KGF-2
10 μg
n=8

FIG.38



EPIDERMAL THICKNESS (μ)
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
p=0.01
54.8
60.5
66.5
59.6
BUFFER
KGF-2
1 μg
KGF-2
4 μg
KGF-2
10 μg

FIG.39

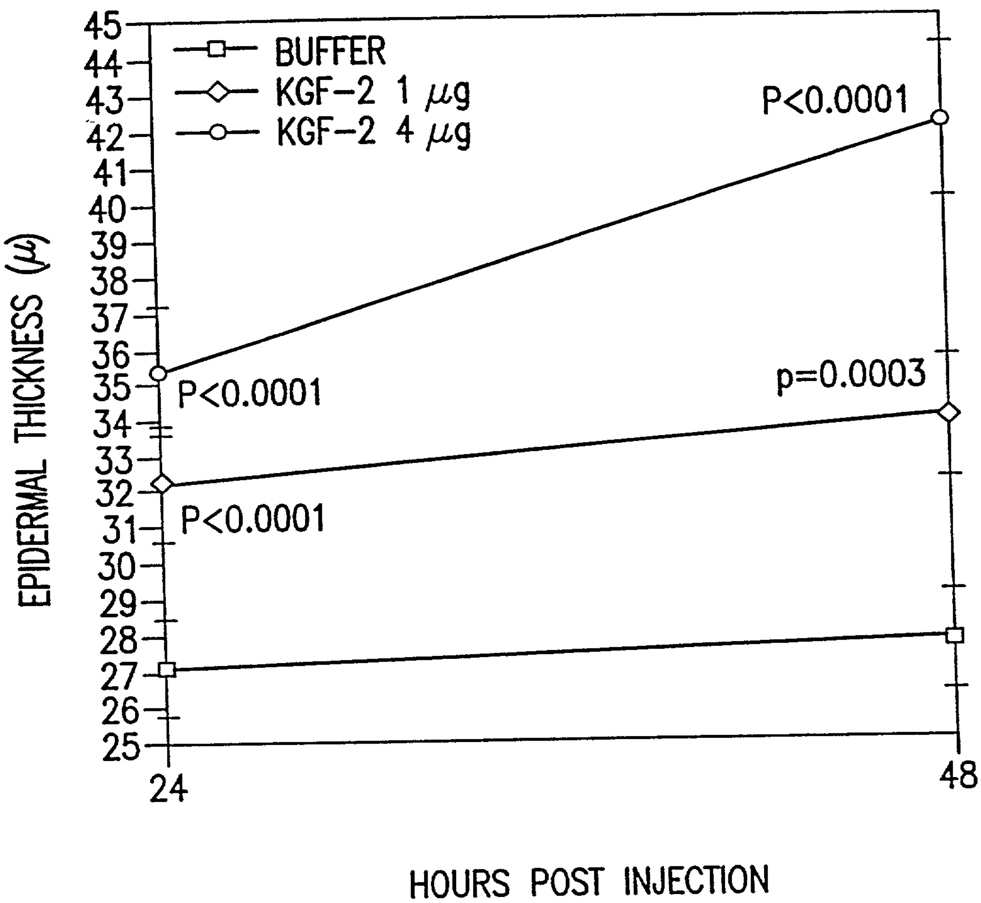
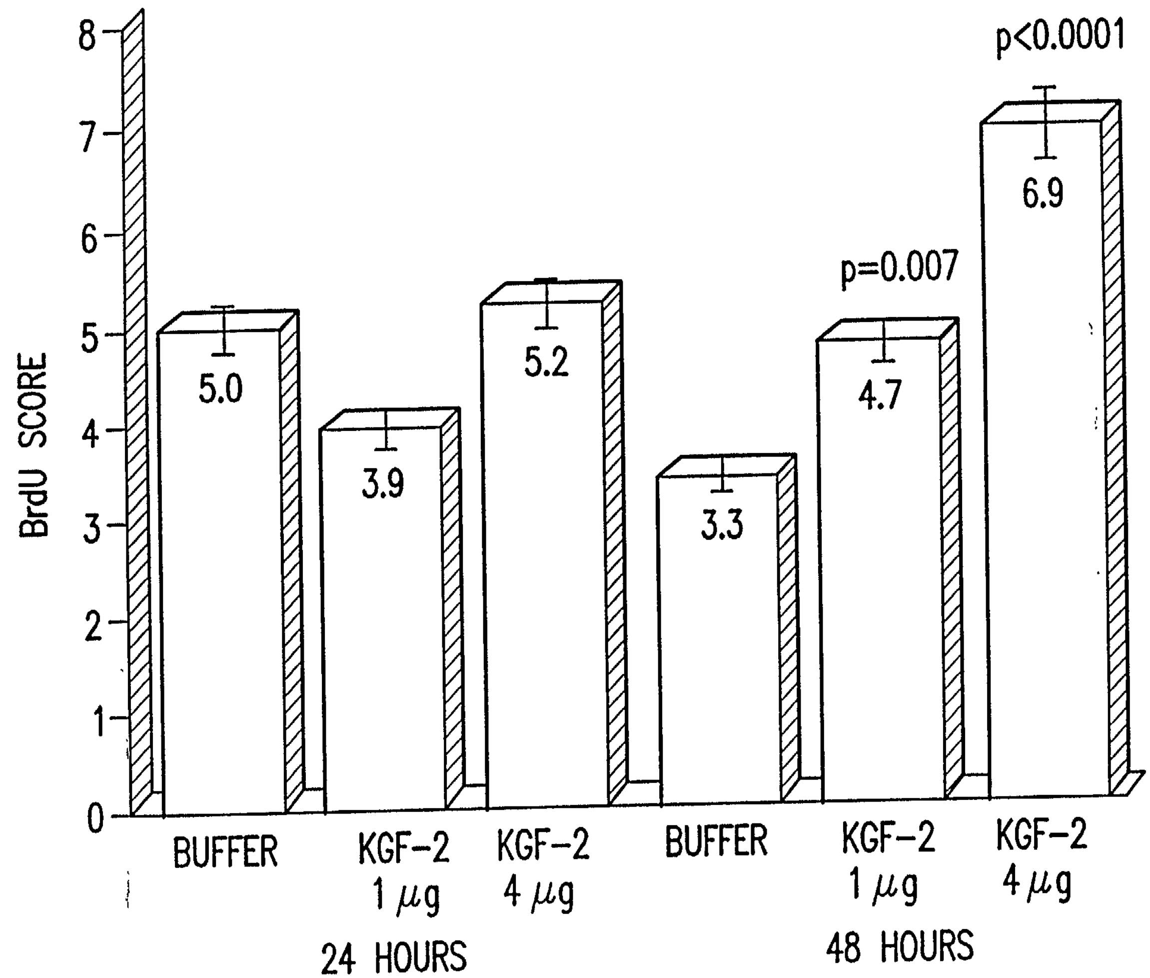

BUFFER
KGF-2 1 μg
KGF-2 4 μg
P<0.0001
P<0.0001
p=0.0003
P<0.0001
EPIDERMAL THICKNESS (μ)
45
44
43
42
41
40
39
38
37
36
35
34
33
32
31
30
29
28
27
26
25
24
48
HOURS POST INJECTION

FIG.40



BrdU SCORE
0
1
2
3
4
5
6
7
8
5.0
3.9
5.2
3.3
4.7
6.9
p=0.007
p<0.0001
BUFFER
KGF-2 1 μg
KGF-2 4 μg
24 HOURS
BUFFER
KGF-2 1 μg
KGF-2 4 μg
48 HOURS

FIG.41

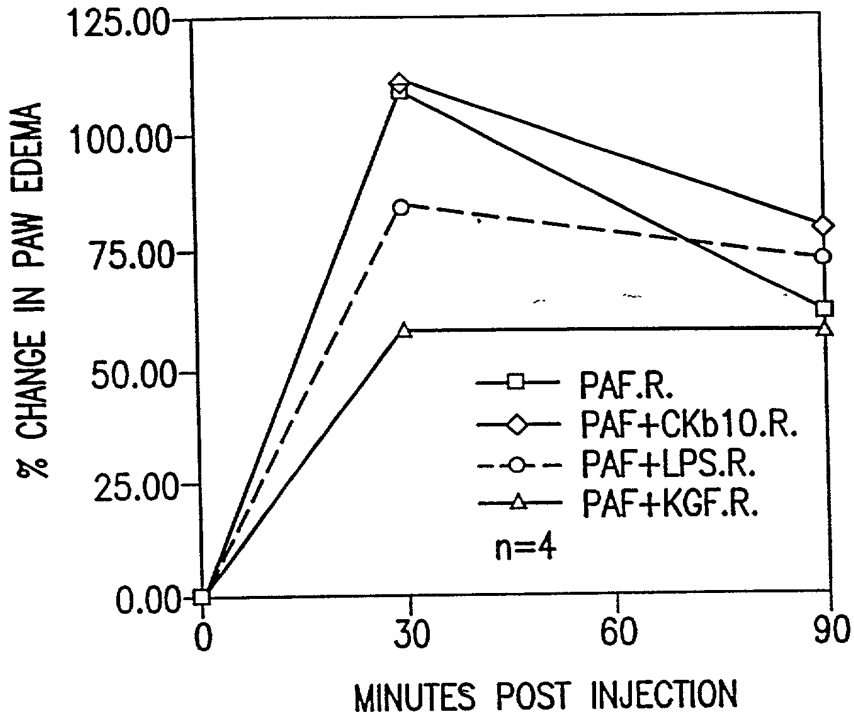


FIG.42A

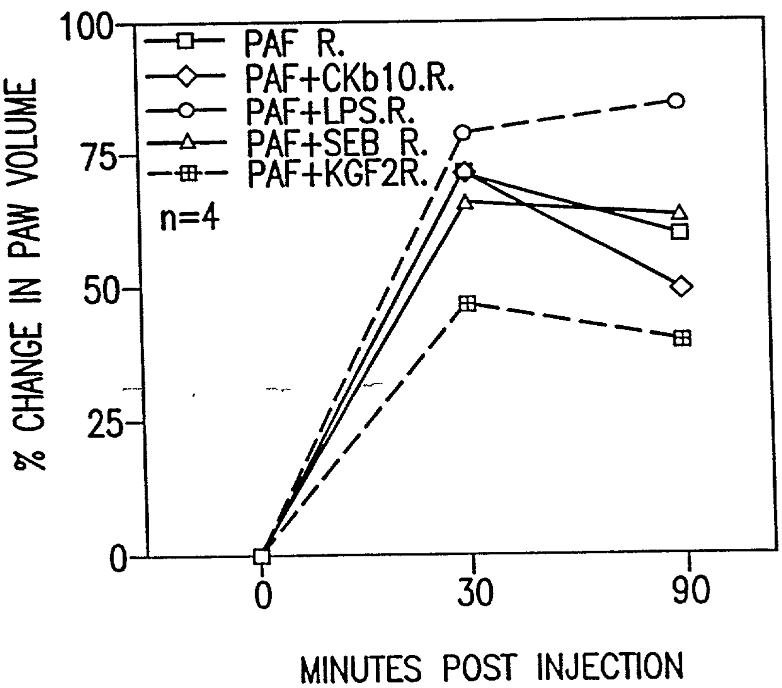


FIG.42B

EFFECT OF KGF-2 Δ33 ON PAF-INDUCED PAW EDEMA IN LEWIS RATS

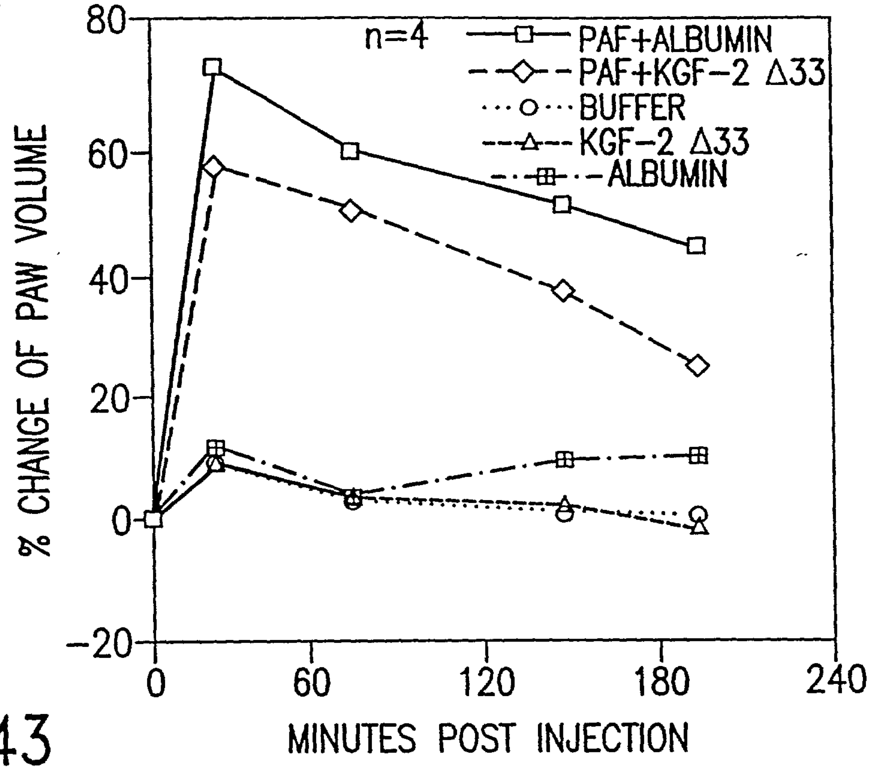


FIG.43

EFFECT OF KGF-2 Δ33 ON SURVIVAL OF WHOLE BODY IRRADIATED Balb/c MICE

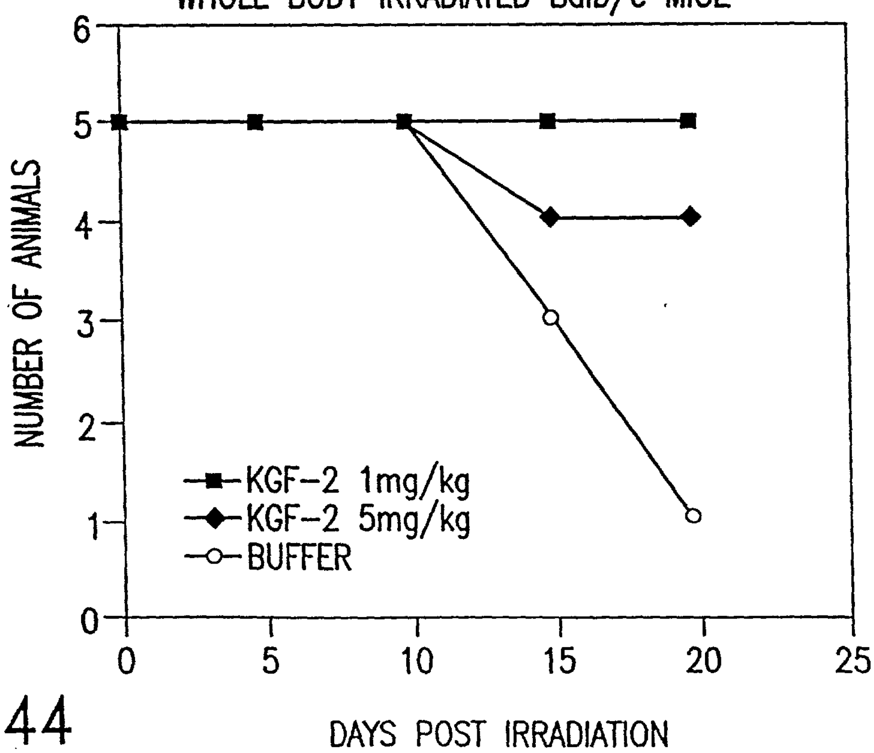


FIG.44

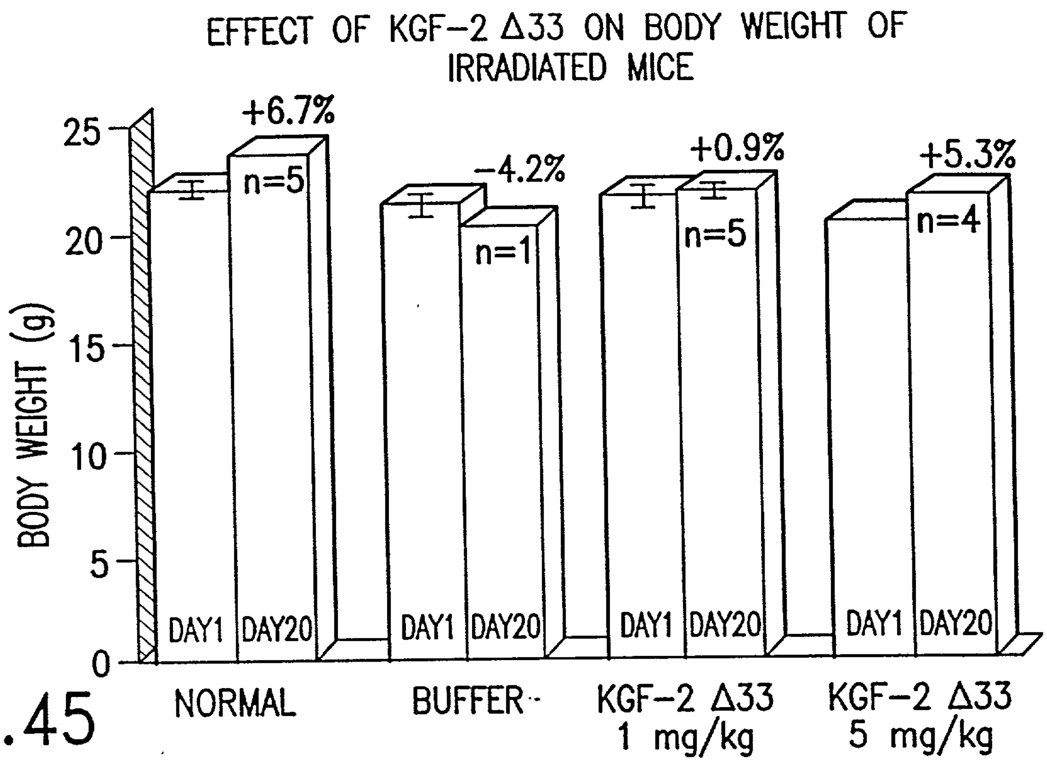

EFFECT OF KGF-2 Δ33 ON BODY WEIGHT OF IRRADIATED MICE
BODY WEIGHT (g)
25
20
15
10
5
0
+6.7%
n=5
-4.2%
n=1
+0.9%
n=5
+5.3%
n=4
DAY1
DAY20
NORMAL
BUFFER
KGF-2 Δ33 1 mg/kg
KGF-2 Δ33 5 mg/kg

FIG.45

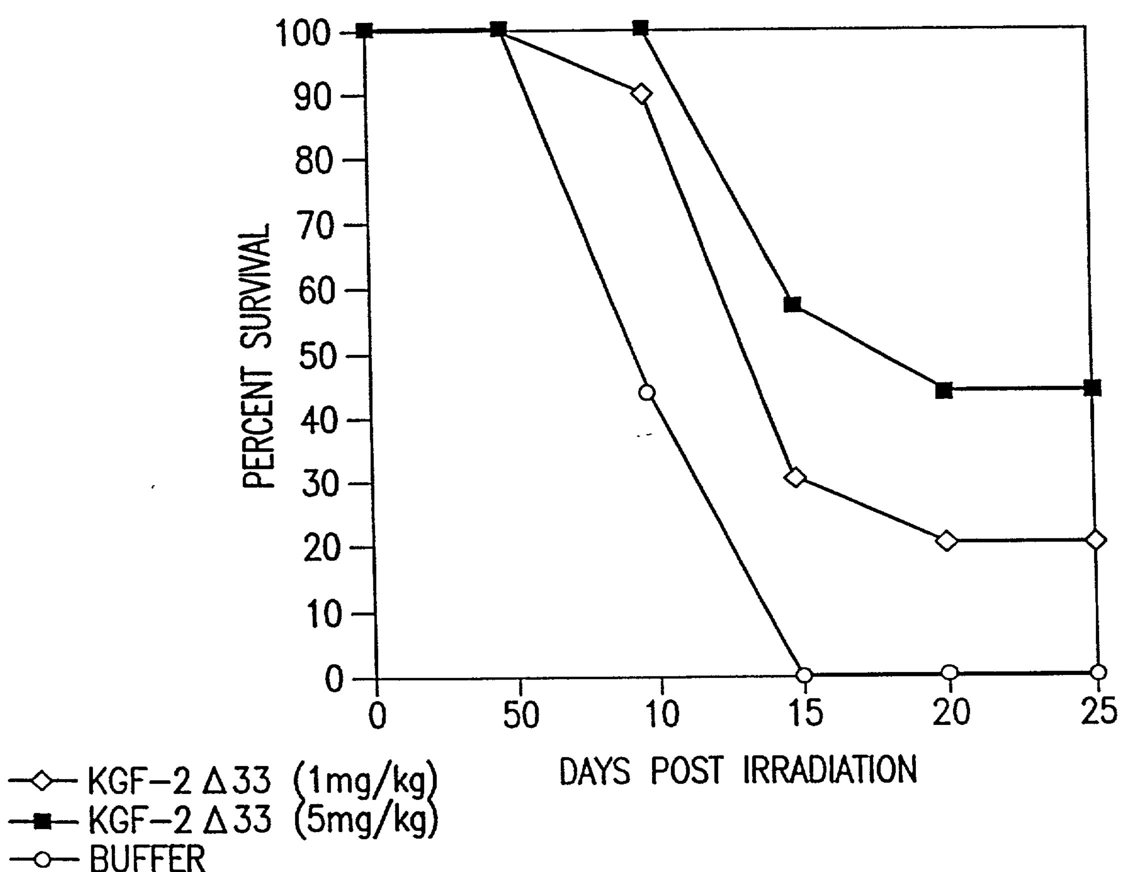

PERCENT SURVIVAL
100
90
80
70
60
50
40
30
20
10
0
0
50
10
15
20
25
DAYS POST IRRADIATION
KGF-2 Δ33 (1mg/kg)
KGF-2 Δ33 (5mg/kg)
BUFFER

FIG.46

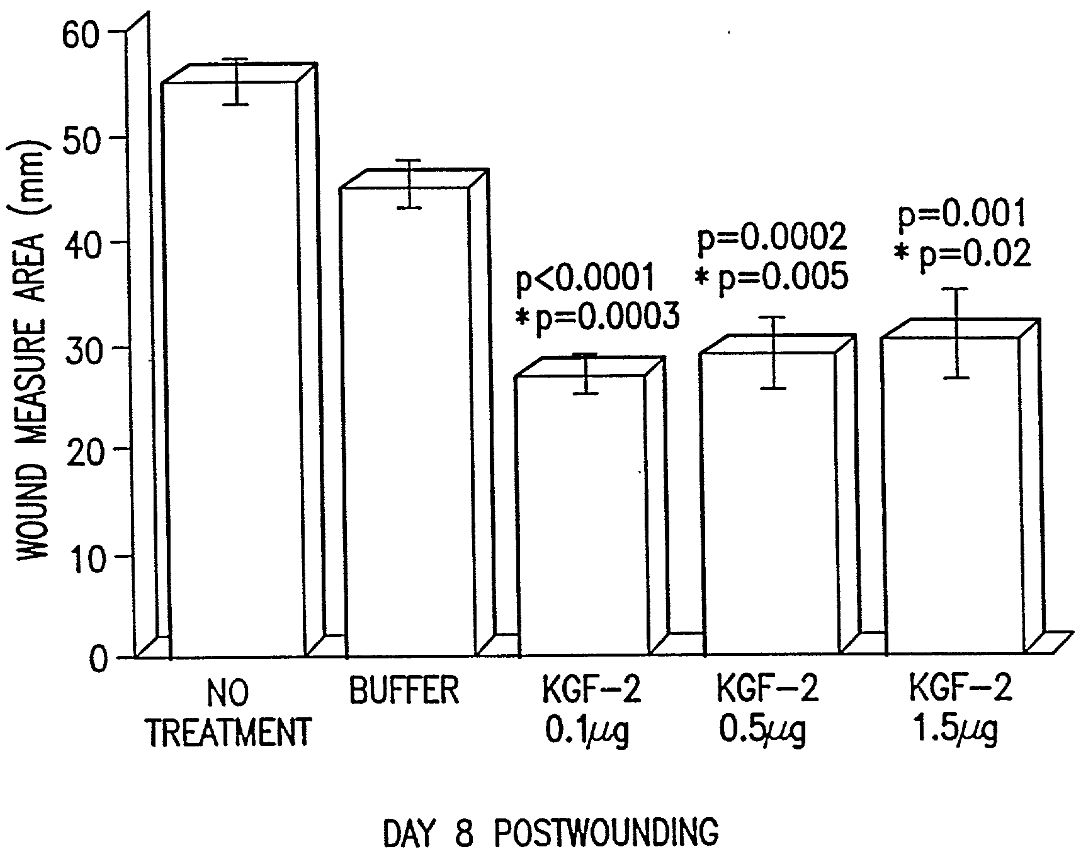
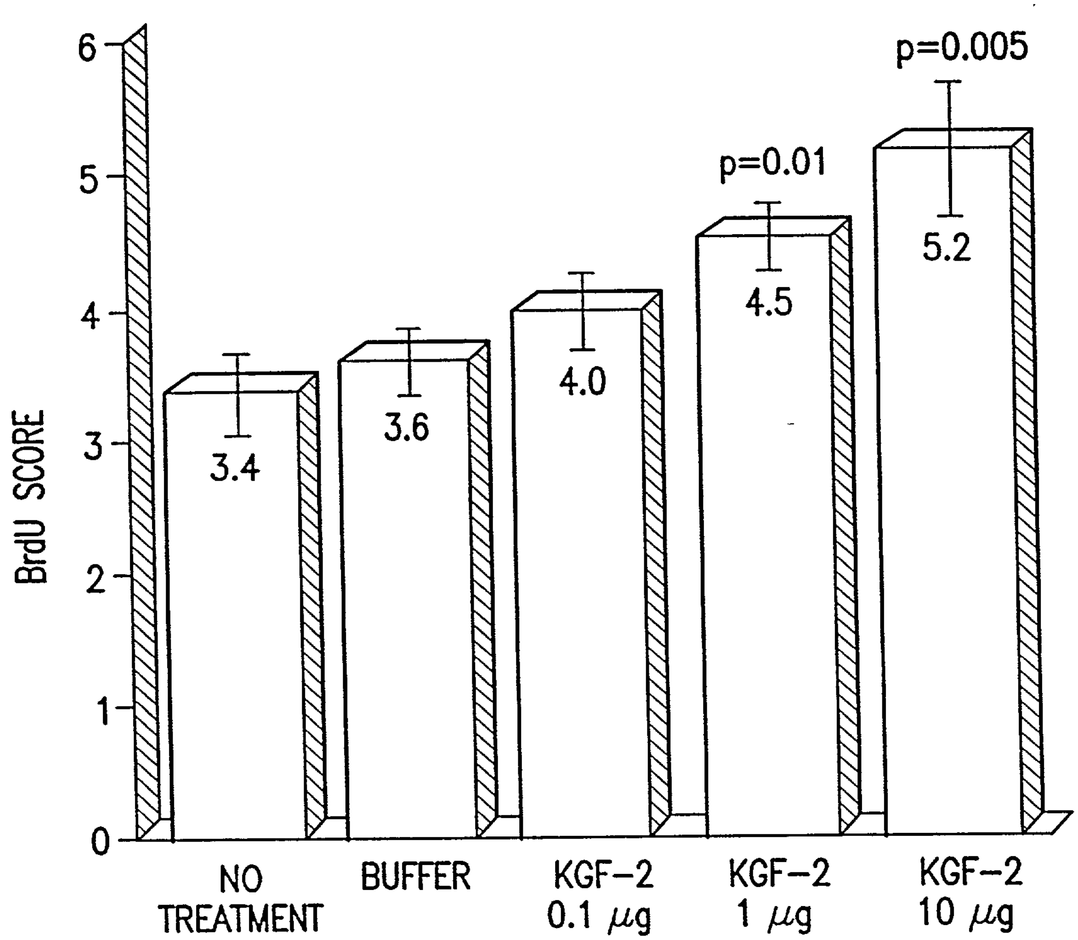

60
50
40
30
20
10
0
WOUND MEASURE AREA (mm)
p<0.0001
*p=0.0003
p=0.0002
*p=0.005
p=0.001
*p=0.02
NO TREATMENT
BUFFER
KGF-2 0.1μg
KGF-2 0.5μg
KGF-2 1.5μg
DAY 8 POSTWOUNDING

FIG.47



p=0.005
p=0.01
6
5
4
3
2
1
0
BrdU SCORE
3.4
3.6
4.0
4.5
5.2
NO TREATMENT
BUFFER
KGF-2 0.1 μg
KGF-2 1 μg
KGF-2 10 μg

FIG.48

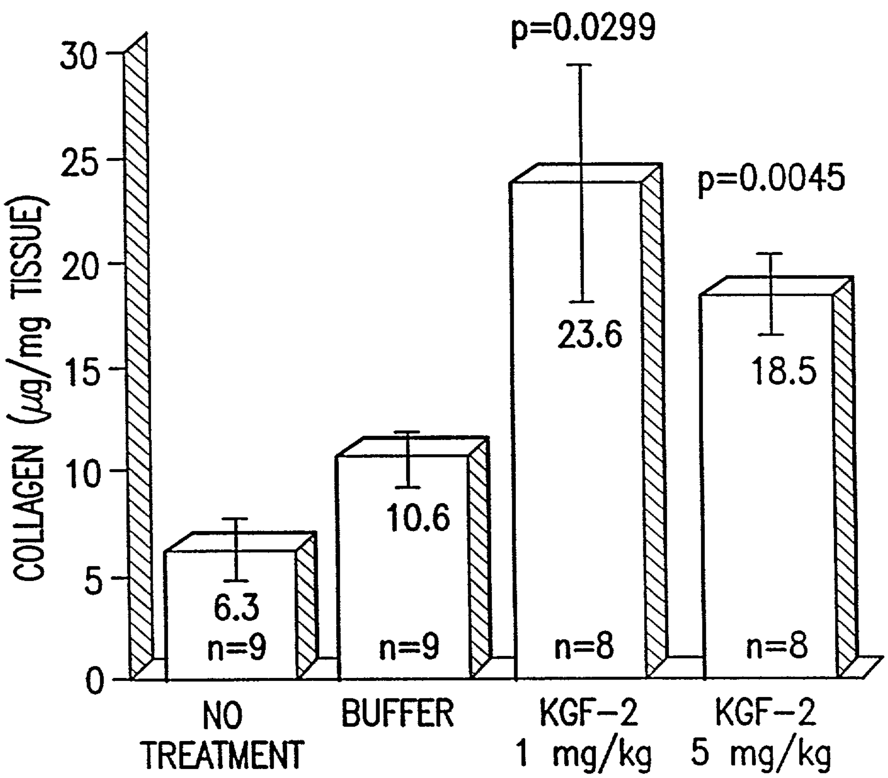

COLLAGEN (μg/mg TISSUE)
30
25
20
15
10
5
0
p=0.0299
p=0.0045
6.3
n=9
10.6
n=9
23.6
n=8
18.5
n=8
NO TREATMENT
BUFFER
KGF-2 1 mg/kg
KGF-2 5 mg/kg

FIG.49

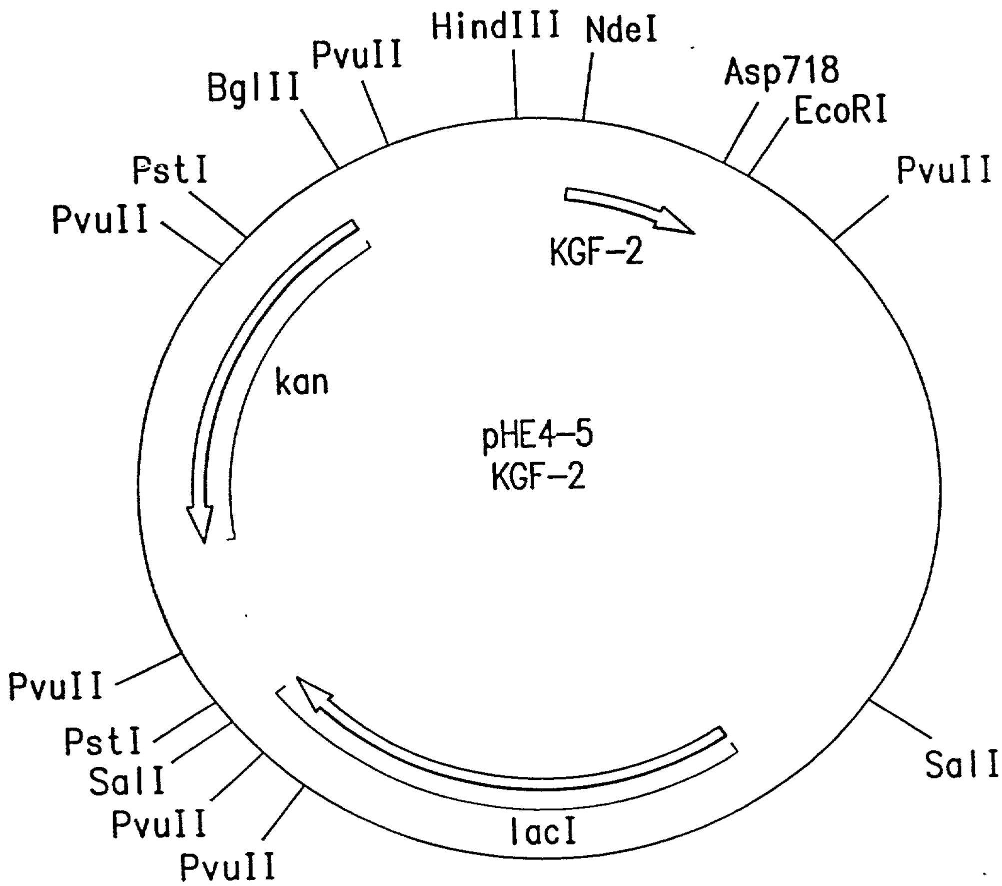

HindIII
NdeI
PvuII
BglII
Asp718
EcoRI
PvuII
PstI
PvuII
KGF-2
kan
pHE4-5
KGF-2
PvuII
PstI
SalI
PvuII
PvuII
lacI
SalI

FIG. 50

−35 Operator 1

1 *AAGCTT* AAAAAACTGCAAAAAATAGTTTGACTTGTGAGCGGATAACAAT

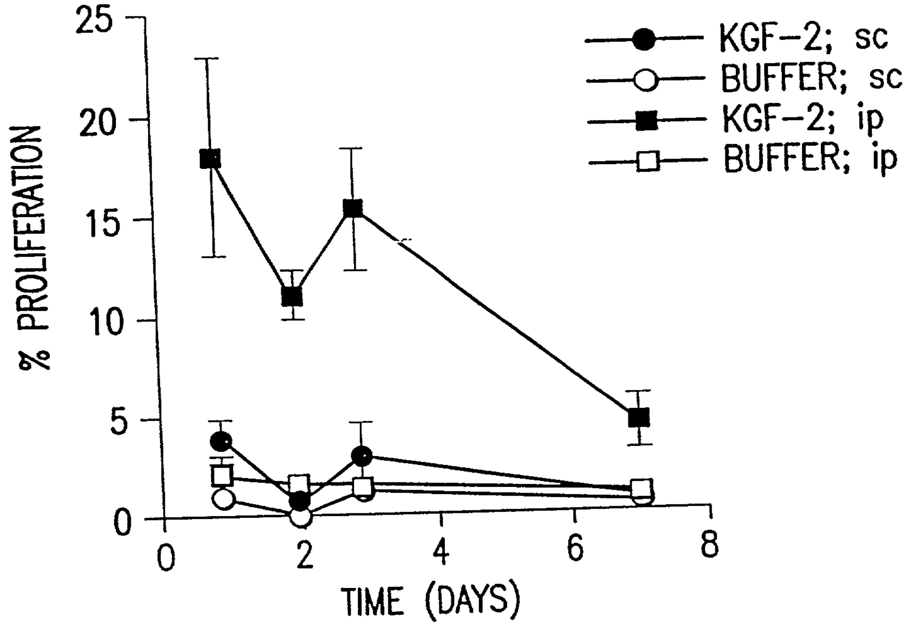
−10 Operator 2

50 TAAGATGTACCCAATTGTGAGCGGATAACAATTTCACACATTAA

S/D

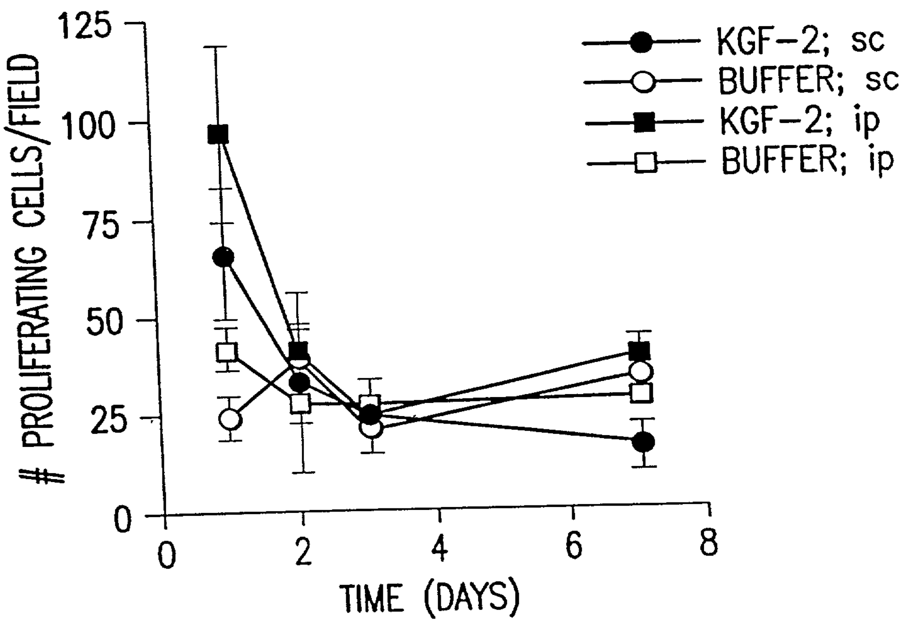
94 AGAGGAGAAATTA *CATATG*

FIG. 51



% PROLIFERATION
25
20
15
10
5
0
0
2
4
6
8
TIME (DAYS)
KGF-2; sc
BUFFER; sc
KGF-2; ip
BUFFER; ip

FIG. 52



PROLIFERATING CELLS/FIELD
125
100
75
50
25
0
0
2
4
6
8
TIME (DAYS)
KGF-2; sc
BUFFER; sc
KGF-2; ip
BUFFER; ip

FIG. 53

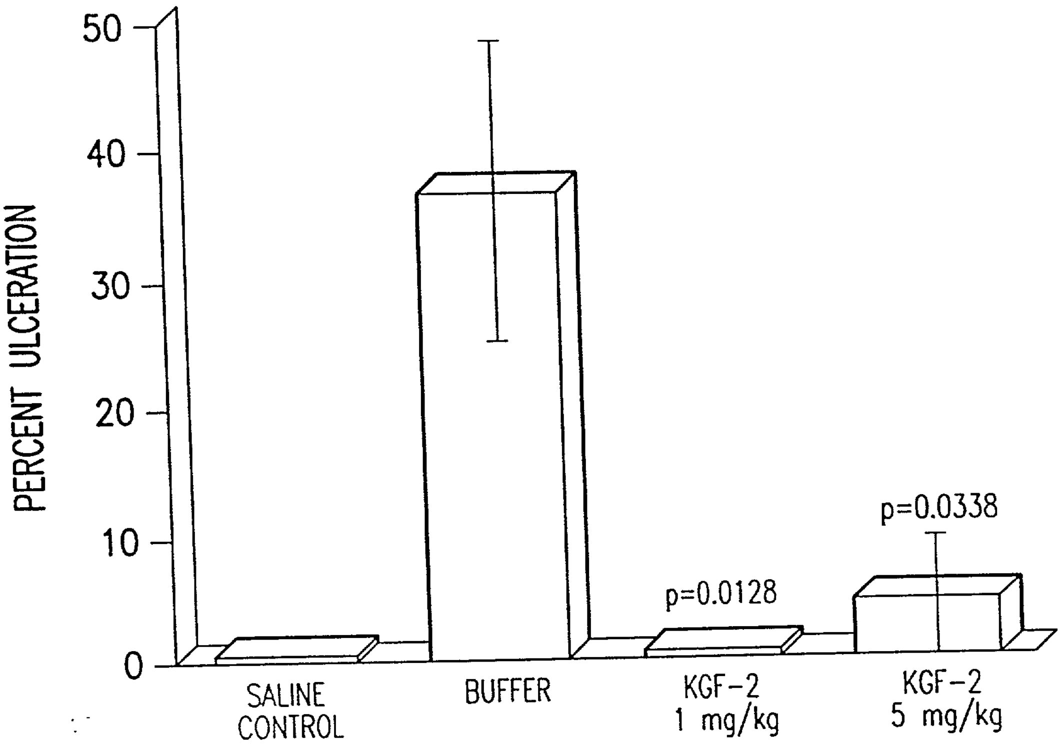

50
40
30
20
10
0
PERCENT ULCERATION
p=0.0128
p=0.0338
SALINE CONTROL
BUFFER
KGF-2 1 mg/kg
KGF-2 5 mg/kg

FIG. 54

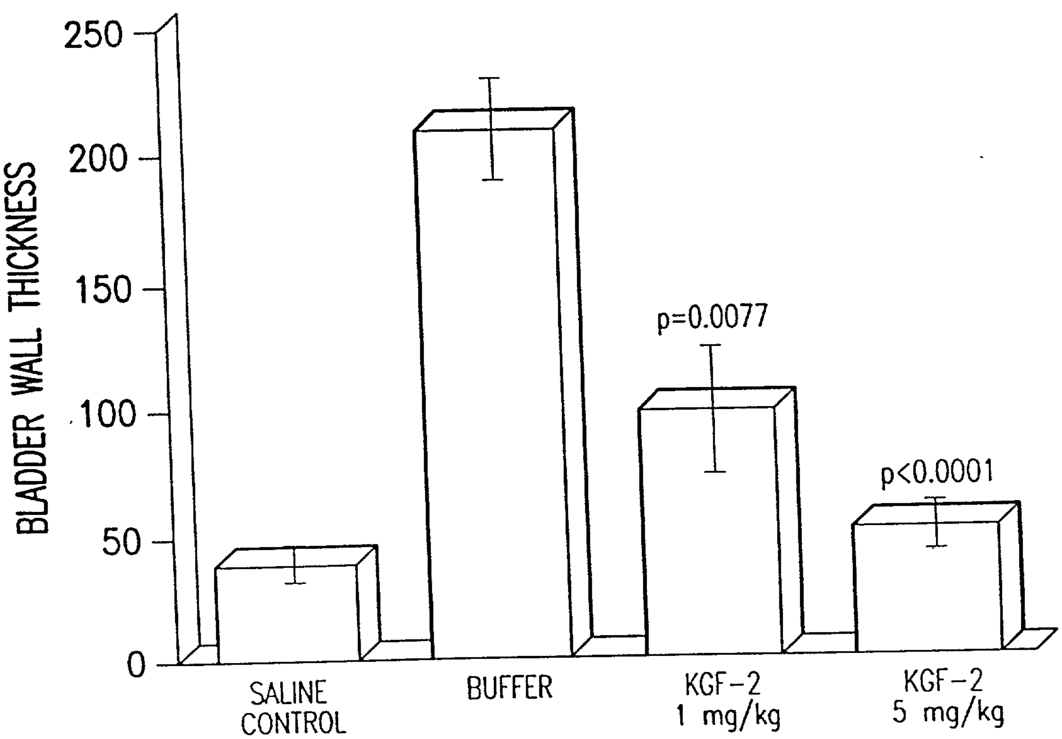

250
200
150
100
50
0
BLADDER WALL THICKNESS
p=0.0077
p<0.0001
SALINE CONTROL
BUFFER
KGF-2 1 mg/kg
KGF-2 5 mg/kg

FIG. 55

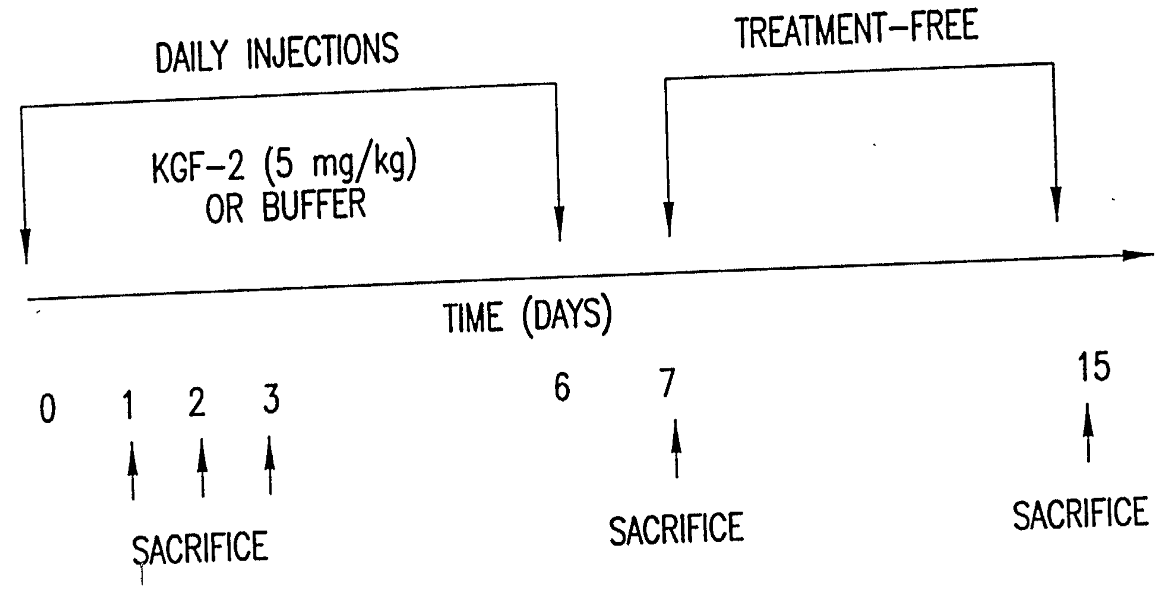

DAILY INJECTIONS
KGF–2 (5 mg/kg)
OR BUFFER
TREATMENT–FREE
TIME (DAYS)
0
1
2
3
6
7
15
SACRIFICE
SACRIFICE
SACRIFICE

FIG. 56

PROLIFERATION OF HEPATOCYTES FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

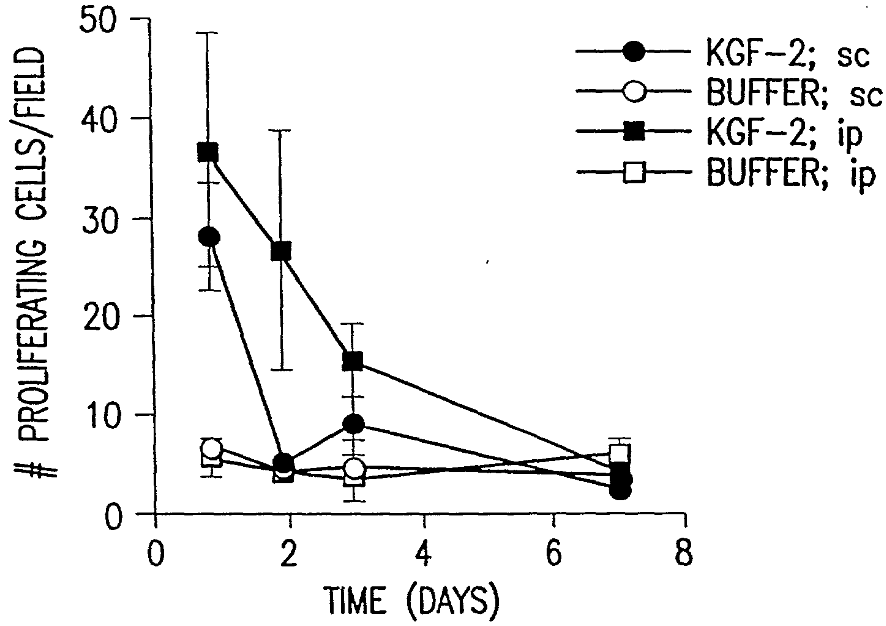


FIG. 57

PROLIFERATION OF PANCREATIC CELLS FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

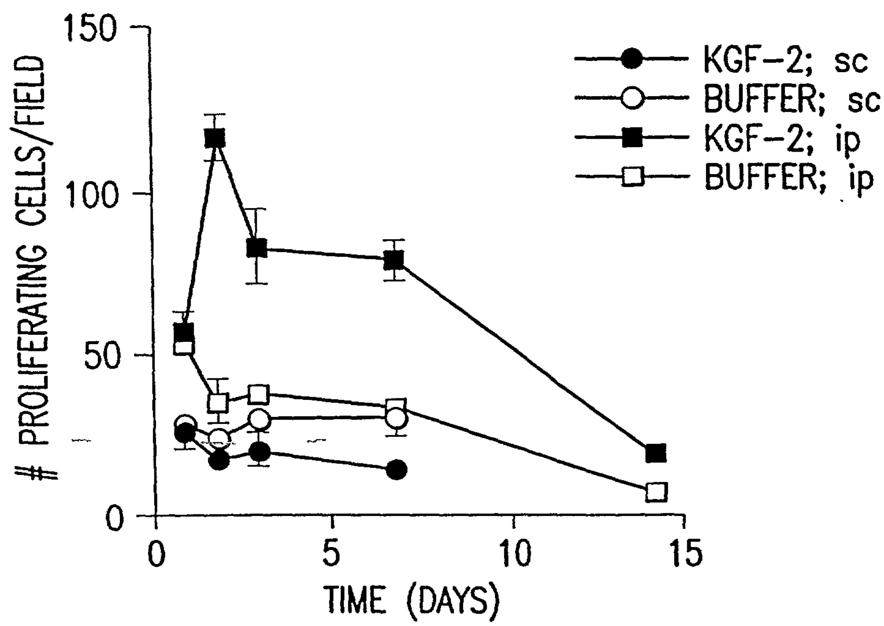


FIG. 58

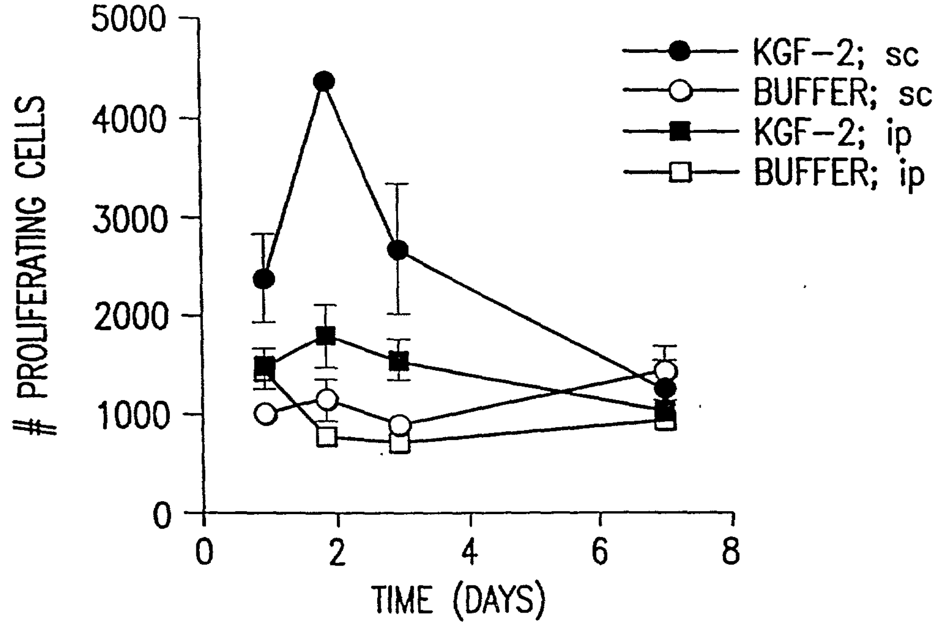

5000
4000
3000
2000
1000
0
PROLIFERATING CELLS
0
2
4
6
8
TIME (DAYS)
KGF-2; sc
BUFFER; sc
KGF-2; ip
BUFFER; ip

FIG. 59

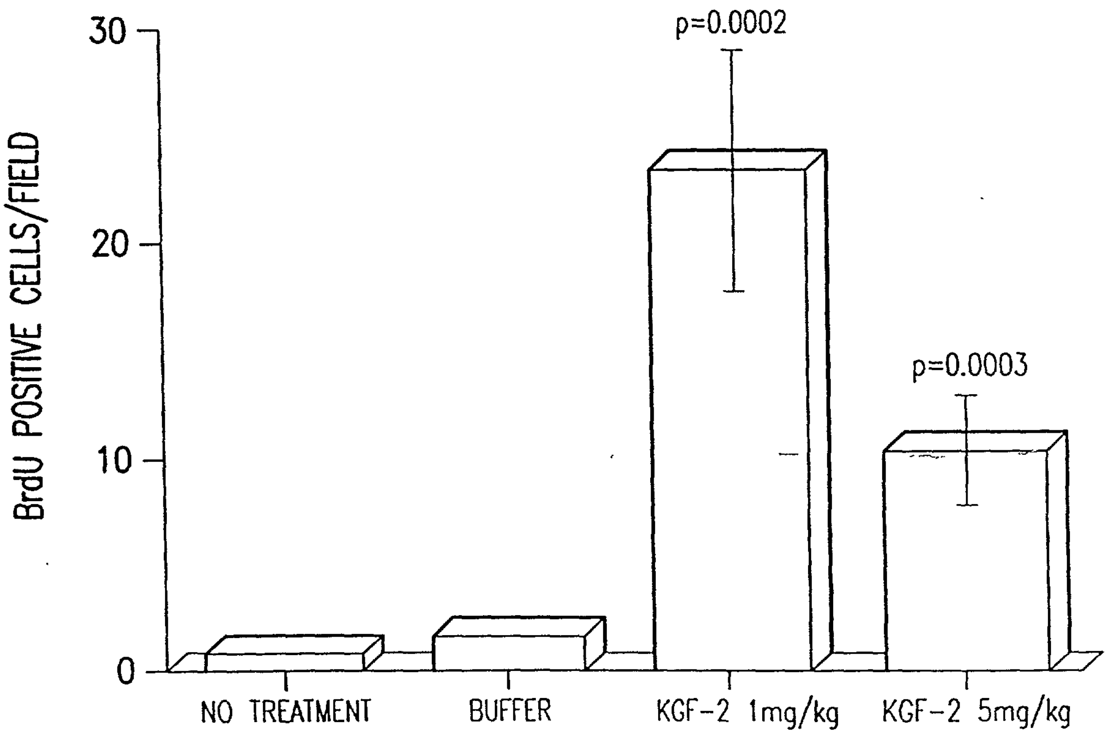

30
20
10
0
BrdU POSITIVE CELLS/FIELD
p=0.0002
p=0.0003
NO TREATMENT
BUFFER
KGF-2 1mg/kg
KGF-2 5mg/kg

FIG. 60